

**MEANS AND METHODS FOR MONITORING PROTEASE
INHIBITOR ANTIRETROVIRAL THERAPY AND GUIDING
THERAPEUTIC DECISIONS IN THE TREATMENT OF HIV/AIDS**

This application is a continuation-in-part and claims priority of U.S. Application No. 09/663,458, filed September 15, 2000, the contents of each of which are hereby incorporated by reference into this application.

Throughout this application, various references are referred to within parenthesis. Disclosures of these publications in their entirety are hereby incorporated by reference into this application to more fully describe the state of the art to which this invention pertains.

Technical Field

This invention relates to antiretroviral drug susceptibility and resistance tests to be used in identifying effective drug regimens for the treatment of human immunodeficiency virus (HIV) infection and acquired immunodeficiency syndrome (AIDS). The invention further relates to the means and methods of monitoring the clinical progression of HIV infection and its response to antiretroviral therapy using phenotypic or genotypic susceptibility assays. The invention also relates to novel vectors, host cells and compositions for carrying out phenotypic susceptibility tests. The invention further relates to the use of various genotypic methodologies to identify patients who do not respond to a particular antiretroviral drug regimen. This invention also relates to the screening of candidate antiretroviral drugs for their capacity to inhibit viral replication,

selected viral sequences and/or viral proteins. More particularly, this invention relates to the determination of protease inhibitor (PRI) susceptibility using phenotypic or genotypic susceptibility tests. This invention also relates to a means and method for accurately and reproducibly measuring viral replication fitness.

Background of the Invention

HIV infection is characterized by high rates of viral turnover throughout the disease process, eventually leading to CD4 depletion and disease progression. Wei X, Ghosh SK, Taylor ME, et al. (1995) Nature 343, 117-122 and Ho DD, Naumann AU, Perelson AS, et al. (1995) Nature 373, 123-126. The aim of antiretroviral therapy is to achieve substantial and prolonged suppression of viral replication. Achieving sustained viral control is likely to involve the use of sequential therapies, generally each therapy comprising combinations of three or more antiretroviral drugs. Choice of initial and subsequent therapy should, therefore, be made on a rational basis, with knowledge of resistance and cross-resistance patterns being vital to guiding those decisions. The primary rationale of combination therapy relates to synergistic or additive activity to achieve greater inhibition of viral replication. The tolerability of drug regimens will remain critical, however, as therapy will need to be maintained over many years.

In an untreated patient, some 10^{10} new viral particles are produced per day. Coupled with the failure of HIV reverse transcriptase (RT) to correct transcription errors by exonucleolytic proofreading, this high level of viral

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turnover results in 10^4 to 10^5 mutations per day at each position in the HIV genome. The result is the rapid establishment of extensive genotypic variation. While some template positions or base pair substitutions may be more error prone (Mansky LM, Temin HM (1995) J Virol 69, 5087-5094) (Schinazi RF, Lloyd RM, Ramanathan CS, et al. (1994) Antimicrob Agents Chemother 38, 268-274), mathematical modeling suggests that, at every possible single point, mutation may occur up to 10,000 times per day in infected individuals.

For antiretroviral drug resistance to occur, the target enzyme must be modified while preserving its function in the presence of the inhibitor. Point mutations leading to an amino acid substitution may result in changes in shape, size or charge of the active site, substrate binding site or in positions surrounding the active site of the enzyme. Mutants resistant to[^] antiretroviral agents have[^] been detected at low levels before the initiation of therapy. (Mohri H, Singh MK, Ching WTW, et al. (1993) Proc Natl Acad Sci USA 90, 25-29) (Nájera I, Richman DD, Olivares I, et al. (1994) AIDS Res Hum Retroviruses 10, 1479-1488) (Nájera I, Holguin A, Quiñones-Mateu E, et al. (1995) J Virol 69, 23-31). However, these mutant strains represent only a small proportion of the total viral load and may have a replication or competitive disadvantage compared with wild-type virus. (Coffin JM (1995) Science 267, 483-489). The selective pressure of antiretroviral therapy provides these drug-resistant mutants with a competitive advantage and thus they come to represent the dominant quasi species (Frost SDW, McLean AR (1994) AIDS 8, 323-332) (Kellam P, Boucher CAB, Tijnagal JMGH (1994) J

Gen Virol 75, 341-351) ultimately leading to a rebound in viral load in the patient.

Early development of antiretroviral therapy focused on inhibitors of reverse transcriptase. Both nucleoside and non-nucleoside inhibitors of this enzyme showed significant antiviral activity (DeClerq, E. (1992) AIDS Res. Hum. Retrovir. 8:119-134). However, the clinical benefit of these drugs had been limited due to drug resistance, limited potency, and host cellular factors (Richman, D.D. (1993) Ann. Rev. Pharm. Tox. 32:149-164). Thus inhibitors targeted against a second essential enzyme of HIV were urgently needed.

In 1988, the protease enzyme of HIV was crystallized and its three-dimensional structure was determined, (Navia MA, Fitzgerald PMD, McKeever BM, Leu CT, Heimbach JC, Herber WK, Sigal IS, Darke PL, Springer JP (1989) Nature 337:615-620 and Winters MA, Schapiro JM, Lawrence J, Merigan TC (1997) In Abstracts of the International Workshop on HIV Drug Resistance, Treatment Strategies and Eradication, St. Petersburg, Fla.) allowing for the rapid development of protease inhibitors. Initially, it was hypothesized that HIV protease, unlike reverse transcriptase, would be unable to accommodate mutations leading to drug resistance. This is not the case, and to date over 20 amino acid substitutions in the HIV protease have been observed during treatment with the currently available protease inhibitors. The genetic pattern of mutations conferring resistance to these protease inhibitors is complex, and cross-resistance between structurally different compounds occurs.

PROTEASE INHIBITORS

HIV protease was classified as an aspartic proteinase on the basis of putative active-site homology (Toh H, Ono M, Saigo K, Miyata T (1985) Nature 315:691), its inhibition by peptastin (Richards AD, Roberts R, Dunn BM, Graves MC, Kay J (1989) FEBS Lett 247:113), and its crystal structure (Navia MA, Fitzgerald PMD, McKeever BM, Lau CT, Heimbach JC, Herber WK, Sigal IS, Darke PL, Springer JP (1989) Nature 337:615-620). The enzyme functions as a homodimer composed of two identical 99-amino acid chains (Debouck C, Navia MA, Fitzgerald PMD, McKeever BM, Leu CT, Heimbach JC, Herber WK, Sigal IS, Darke PL, Springer JP (1988) Proc. Natl. Acad. Sci. USA 84:8903-8906), with each chain containing the characteristic Asp-Thr-Gly active-site sequence at positions 25 to 27 (Toh H, Ono M, Saigo K, Miyata T (1985) Nature 315:691).

HIV protease processes gag (p55) and gag-pol (p160) polyprotein products into functional core proteins and viral enzymes (Kohl NE, Diehl RE, Rands E, Davis LJ, Hanobik MG, Wolanski B, Dixon RA (1991) J. Virol. 65:3007-3014 and Kramer RA, Schaber MD, Skalka AM, Ganguly K, Wong-Staal F, Reddy EP (1986) Science 231:1580-1584). During or immediately after budding, the polyproteins are cleaved by the enzyme at nine different cleavage sites to yield the structural proteins (p17, p24, p7, and p6) as well as the viral enzymes reverse transcriptase, integrase, and protease (Pettit SC, Michael SF, Swanstrom R (1993) Drug Discov. Des. 1:69-83).

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An asparagine replacement for aspartic acid at active-site residue 25 results in the production of noninfectious

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viral particles with immature, defective cores (Huff JR
(1991) AIDS J. Med. Chem. 34:2305-2314, Kaplan AH, Zack
JA, Knigge M, Paul DA, Kempf DJ, Norbeck DW, Swanstrom R
(1993) J. Virol. 67:4050-4055, Kohl NE, Emini EA, Schleif
5 WA, Davis LJ, Heimbach JC, Dixon RA, Scolnik EM, Sigal IS
(1988) Proc. Natl. Acad. Sci. USA 85:4686-4690, Peng C, Ho
BK, Chang TW, Chang NT (1989) J. Virol. 63:2550-2556).
Similarly, wild-type virus particles produced by infected
cells treated with protease inhibitors contain unprocessed
10 precursors and are noninfectious (Crawford S, Goff SP
(1985) J. Virol. 53:899-907, Gottlinger HG, Sodroski JG,
Haseltine WA (1989) Proc. Natl. Acad. Sci. USA
86:5781-5785, Katoh IY, Yoshinaka Y, Rein A, Shibuya M,
Odaka T, Oroszlan S (1985) Virology 145:280-292, Kohl NE,
15 Emini EA, Schleif WA, Davis LJ, Heimbach JC, Dixon RA,
Scolnik EM, Sigal IS (1988) Proc. Natl. Acad. Sci. USA
85:4686-4690, Peng C, Ho BK, Chang TW, Chang NT (1989) J.
Virol. 63:2550-2556, Stewart L, Schatz G, Wogt VM (1990)
J. Virol. 64:5076-5092). Unlike reverse transcriptase
20 inhibitors, protease inhibitors block the production of
infectious virus from chronically infected cells (Lambert
DM, Petteway, Jr. SR, McDaniel CE, Hart TK, Leary JJ,
Dreyer GB, Meek TD, Bugelski PJ, Bolognesi DP, Metcalf BW,
Matthews TJ (1992) Antibicrob. Agents Chemother.
25 36:982-988). Although the viral protease is a symmetric
dimer, it binds its natural substrates or inhibitors
asymmetrically (Dreyer, GB, Boehm JC, Chenere B,
DesJarlais RL, Hassell AM, Meek TD, Tomaszek TAJ, Lewis M
(1993) Biochemistry 32:937-947, Miller MJ, Schneider J,
30 Sathyanarayana BK, Toth MV, Marshall GR, Clawson L, Selk
L, Kent SB, Wlodawer A (1989) Science 246:1149-1152).
These findings together with the knowledge that amide

bonds of proline residues are not susceptible to cleavage by mammalian endopeptidases gave rise to the first class of HIV-1 protease inhibitors based on the transition state mimetic concept, with the phenylalanine-proline cleavage site being the critical nonscissile bond (Roberts NA, Martin JA, Kinchington D, Broadhurst AV, Craig JC, Duncan IB, Galpin SA, Handa BK, Kay J, Krohn A, Lambert RW, Merett JH, Mills JS, Parkes KEB, Redshaw S, Ritchie AJ, Taylor DL, Thomas GJ, Machin PJ (1990) Science 248:358-361).

Amino acids implicated in resistance to protease inhibitors.

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~~As new protease inhibitors are developed, the ability of certain amino acid substitutions to confer resistance to the inhibitor is usually determined by several methods, including selection of resistant strains in vitro, site-directed mutagenesis, and determination of amino acid changes that are selected during early phase clinical trials in infected patients. While some amino acid substitutions are specifically correlated with resistance to certain protease inhibitors (see below), there is considerable overlap between sets of mutations implicated in resistance to all approved protease inhibitors. Many investigators have attempted to classify these mutations as either being "primary" or "secondary", with varying definitions. For example, some investigators classify as primary mutations which are predicted, based on X-ray crystallographic data, to be in the enzyme active site with the potential for direct contact with the inhibitor (e.g. D30N, G48V, I50V, V82A/F/S/T, I84V, N88S, L90M).~~

Secondary mutations are usually considered as being compensatory for defects in enzyme activity imposed by primary mutations, or as having enhancing effects on the magnitude of resistance imparted by the primary mutations (e.g. L10I/F/R/V, K20I/M/R/T, L24I, V32I, L33F/V, M36I/L/V, M46I/L/V, I47V, I54L/V, L63X, A71T/V, G73A/S/T, V77I, N88D). Lists of mutations and corresponding inhibitors are maintained by several organizations, for example: Schinazi et al., Mutations in retroviral genes associated with drug resistance, *Intl. Antiviral News* 1999, 7:46-69 and Shafer et al., Human Immunodeficiency Virus Reverse Transcriptase and Protease Sequence Database, *Nucleic Acids Research* 1999, 27(1), 348-352 (also accessible via the internet at <http://www.viral-resistance.com/> or <http://hivdb.stanford.edu/hiv/>)

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Saquinavir

5 Saquinavir, developed by Hoffmann-La Roche, was the first
protease inhibitor to undergo clinical evaluation,
demonstrating that HIV-1 protease was a valid target for
the treatment of HIV infection (Jacobsen H, Brun-Vezinet
F, Duncan I, Hanggi M, Ott M, Vella S, Weber J, Mous J
(1994) J. Virol. 68:2016-2020). Saquinavir is a highly
active peptidomimetic protease inhibitor with a 90%
inhibitory concentration (IC90) of 6 nM (id). In vitro,
10 saquinavir can select for variants with one or both of two
amino acid substitutions in the HIV-1 protease gene, a
valine-for-glycine substitution at position 48 (G48V), a
methionine-for-leucine substitution at residue 90 (L90M),
and the double substitution G48V-L90M (Eberle J, Bechowsky
15 B, Rose D, Hauser U, vonder Helm K, Guertler L, Nitschko H
(1995) AIDS Res. Hum. Retroviruses 11:671-676, Jacobsen H,
Yasargil K, Winslow DL, Craig JC, Kroehn A, Duncan IB,
Mous J (1995) Virology 206:527-534, Turriziani O,
Antonelli G, Jacobsen H, Mous J, Riva E, Pistello M,
20 Dianzani F (1994) Acta Virol. 38:297-298). In most cases,
G48V is the first mutation to appear, and continued
selection results in highly resistant double-mutant
variants. A substitution at either residue results in a
3- to 10-fold decreased susceptibility to the inhibitor,
25 whereas the simultaneous occurrence of both substitutions
causes a more severe loss of susceptibility of >100-fold
(id).

In vivo, saquinavir therapy appears to select almost
exclusively for mutations at codons 90 and 48 (id,
30 Jacobsen H, Hangi M, Ott M, Duncan IB, Owen S, Andreoni M,
Vella S, Mous J (1996) J. Infect. Dis. 173:1379-1387,
Vella S, Galluzzo C, Giannini G, Pirillo MF, Duncan I,

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Jacobsen H, Andreoni M, Sarmati L, Ercoli L (1996) Antiviral Res. 29:91-93). Saquinavir-resistant variants emerge in approximately 45% of patients after 1 year of monotherapy with 1,800 mg daily (Craig IC, Duncan IB, Roberts NA, Whittaker L (1993) In Abstracts of the 9th International Conference on AIDS, Berlin, Germany, Duncan IB, Jacobsen H, Owen S, Roberts NA (1996) In Abstracts of the 3rd Conference of Retroviruses and Opportunistic Infections, Washington, D.D., id, Mous J, Brun-Vezinet F, Duncan IB, Haenggi M, Jacobsen H, Vella S (1994) In Abstracts of the 10th International Conference on AIDS, Yokohama, Japan). The frequency of resistance is lower (22%) in patients receiving combination therapy with zidovudine, zalcitabine, and saquinavir (Collier AC, Coombs R, Schoenfeld DA, Bassett RL, Joseph Timpone MS, Baruch A, Jones M, Facey K, Whitacre C, McAuliffe VJ, Friedman HM, Merigan TC, Reichmann RC, Hooper C, Corey L (1996) N. Engl. J. Med. 334:1011-1017). In contrast to in vitro-selected virus, where the G48V mutation is the first step to resistance, the L90M exchange is the predominant mutation selected in vivo while the G48V (2%) or the double mutant (<2%) is rarely found (id). In another recent study of in vivo resistance during saquinavir monotherapy no patient was found to harbor a G48V mutant virus (Ives KJ, Jacobsen H, Galpin SA, Garaev MM, Dorrell L, Mous J, Bragman K, Weber JN (1997 J. Antimicrob. Chemother. 39:771-779). Interestingly, Winters et al. (id) observed a higher frequency of the G48V mutation in patients receiving higher saquinavir doses as monotherapy. All patients (six of six) who initially developed G48V also acquired a V82A mutation either during saquinavir treatment or after switching to either indinavir or

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nelfinavir. An identical mutational pattern was found in another study during saquinavir monotherapy (Eastman PS, Duncan IB, Gee C, Race E (1997) In Abstracts of the International Workshop on HIV Drug Resistance, Treatment Strategies and Eradication, St. Petersburg, Fla.). Some residues represent sites of natural polymorphism of the HIV-1 protease (positions 10, 36, 63, and 71) and appear to be correlated to the L90M mutation (id). Another substitution, G73S, has been recently identified and may play a role in saquinavir resistance in vivo. Isolates from five patients with early saquinavir resistance and those from two patients with induced saquinavir resistance after a switch of therapy to indinavir carried the G73S and the L90M substitutions Dulioust A, Paulous S, Guillemot L, Boue F, Galanaud P, Clavel F (1997) In Abstracts of the International Workshop on HIV Drug Resistance, Treatment Strategies and Eradication, St. Petersburg, Fla.).

20 **Ritonavir**

Ritonavir, developed by Abbott Laboratories, was the second HIV protease inhibitor to be licensed in the United States. Ritonavir is a potent and selective inhibitor of HIV protease that is derived from a C2-symmetric, peptidomimetic inhibitor (Ho DD, Toyoshima T, Mo H, Kempf DJ, Norbeck D, Chen CM, Wideburg NE, Burt SK, Erickson JW, Singh MK (1994) J. Virol. 68:2016-2020). In vitro activity has been demonstrated against a variety of laboratory strains and clinical isolates of HIV-1 with IC90s of 70 to 200 nM (Kuroda MJ, El-Farrash MA, Clouthury S, Harada S (1995) Virology 210:212-216).

Resistant virus generated by serial in vitro passages is associated with specific mutations at positions 84, 82, 71, 63, and 46 (Markowitz M, Mo H, Kempf DJ, Norbeck DW, Bhat TN, Erickson JW, Ho DD (1995) J. Virol. 69:701-706).

5 The I84V substitution appeared to be the major determinant of resistance, resulting in a 10-fold reduction in sensitivity to ritonavir. Addition of the V82F mutation confers an even greater level of resistance, up to 20-fold. The substitutions M46I, L63P, and A71V, when
10 introduced into the protease coding region of wild-type NL4-3, did not result in significant changes in drug susceptibility. Based on replication kinetics experiments, these changes are likely to be compensatory for active-site mutations, restoring the impaired
15 replicative capacity of the combined V82F and I84V mutations.

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Indinavir

Indinavir, developed by Merck & Co., is the third HIV protease inhibitor licensed in the United States. Indinavir is a potent and selective inhibitor of HIV-1 and HIV-2 proteases with K_i values of 0.34 and 3.3 nM, respectively (Vacca Jp, Dorsey BD, Schleif WA, Levin RB, McDaniel SL, Darke PL, Zugay J, Quintero JC, Blahy OM, Roth E, Sardana VV, Schlabach AJ, Graham PI, Condra JH, Gotlib L, Holloway MK, Lin J, Chen L-w, Vastag K, Ostobich D, Anderson PS, Emini EA, Huff JR (1994) Proc. Natl. Acad. Sci. USA 91:4096-4100). The drug acts as peptidomimetic transition state analogue and belongs to the class of protease inhibitors known as HAPA (hydroxyaminopentane amide) compounds (ibid). Indinavir provides enhanced aqueous solubility and oral bioavailability and in cell culture exhibits an IC_{95} of 50 to 100 nM (Emini EA, Schleif WA, Deutsch P, Condra JH (1996) Antiviral Chemother. 4:327-331.

Despite early reports of a lack of in vitro resistance by selection with indinavir (id), Tisdale et al. (Tisdale M, Myers RE, Maschera B, Parry NR, Oliver NM, Blair ED (1995) Antibicrob. Agents Chemother. 39:1704-1710) were able to obtain resistant variants during selection in MT-4 cells with substitutions at residues 32, 46, 71, and 82. At least four mutations were required to produce a significant loss of susceptibility (6.1-fold compared with the wild type). The mutation at position 71, described as compensatory (Markowitz M, Mo H, Kempf DJ, Norbeck DW, Bhat TN, Erickson JW, Ho DD (1995) J. Virol. (id), appeared to contribute phenotypic resistance and also to improve virus growth. Emini et al. (id) and Condra et al.

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(Condra JH, Holder DJ, Schleif WA, Blahy OM, Danovich RM, Gabryelski LJ, Graham DJ, Laird D, Quintero JC, Rhodes A, Robbins HL, Roth E, Shivaprakash M, Yang T, Chodakewitz JA, Deutsch PJ, Leavitt RY, Massari Fe, Mellors JW, Squires KE, Steigbigel RT, Teppler H, Emini EA (1995) Nature 374:569-571) found by constructing mutant HIV-1 clones that at least three mutations at residues 46, 63, and 82 were required for the phenotypic manifestation of resistance with a fourfold loss of susceptibility.

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Nelfinavir

Nelfinavir, developed by Agouron Pharmaceuticals, is a selective, nonpeptidic HIV-1 protease inhibitor that was designed by protein structure-based techniques using iterative protein crystallographic analysis (Appelt KR, Bacquet J, Bartlett C, Booth CLJ, Freer ST, Fuhry MM, Gehring MR, Herrmann SM, Howland EF, Janson CA, Jones TR, Kan CC, Kathardekar V, Lewis KK, Marzoni GP, Mathews DA, Mohr C, Moomaw EW, Morse CA, Oatley SJ, Ogden RC, Reddy MR, Reich SH, Schoettlin WS, Smith WW, Varney MD, Villafranca JE, Ward RW, Webber S, Webber SE, Welsh KM, White J (1991) J. Med. Chem. 34:1925-1928). In vitro, nelfinavir was found to be a potent inhibitor of HIV-1 protease with a K_i of 2.0 nM (Kaldor SW, Kalish VJ, Davies JF, Shetty BV, Fritz JE, Appelt K, Burgess JA, Campanale KM, Chirgadze NY, Clawson DK, Dressman BA, Hatch SD, Khalil DA, Kosa MB, Lubbehusen PP, Muesing MA, Patrick AK, Reich SH, Su KS, Tatlock JH (1997) J. Med. Chem. 40:3979-3985). The drug demonstrated antiviral activity against several laboratory and clinical HIV-1 and HIV-2 strains with 50% effective concentrations ranging from 9 to 60 nM (Patick AK, Boritzki TJ, Bloom LA (1997) Antimicrob. Agents Chemother. 41:2159-2164). Nelfinavir exhibits additive-to-synergistic effects when combined with other antiretroviral drugs (Partaledis JA, Yamaguchi AK, Tisdale M, Blair EE, Falcione C, Maschera B, Myers RE, Pazhanisamy S, Futer O, Bullinan AB, Stuver CM, Byrn RA, Livingston DJ (1995) J. Virol. 69:5228-5235). Preclinical data showed high levels of the drug in mesenteric lymph nodes and the spleen and good oral bioavailability (Shetty BV, Kosa MB, Khalil DA, Webber S (1996) Antimicrob. Agents Chemother. 40:110-114).

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In vitro, following 22 serial passages of HIV-1_{NL4-3} in the presence of nelfinavir, a variant (P22) with a sevenfold reduced susceptibility was isolated. After an additional six passages a variant (P28) with a 30-fold-decreased susceptibility to nelfinavir was identified (Patick AK, Ho H, Markowitz M, Appelt K, Wu B, Musick L, Kaldor S, Reich S, Ho D, Webber S (1996) Antimicrob. Agents Chemother. 40:292-297). Sequence analysis of the protease gene from these variants identified in decreasing frequency the substitutions D30N, A71V, and I84V for the P22 variant and mutations M46I, I84V/A, L63P, and A71V for the P28 variant. Antiviral susceptibility testing of recombinant mutant HIV-1_{NL4-3} containing various mutations resulted in a fivefold-increased 90% effective concentration for the I84V and D30N single mutants and the M46I/I84V double mutant, whereas no change in susceptibility was observed with M46I, L63P, or A71V alone (*ibid*).

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Amprenavir

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Amprenavir is a novel protease inhibitor developed by Vertex Laboratories and designed from knowledge of the HIV-1 protease crystal structure (Kim EE, Baker CT, Dyer MD, Murcko MA, Rao BG, Tung RD, Navia MA (1995) J. Am. Chem. Soc. 117:1181-1182). The drug belongs to the class of sulfonamide protease inhibitors and has been shown to be a potent inhibitor of HIV-1 and HIV-2, with IC50s of 80 and 340 nM, respectively. The mean IC50 for amprenavir against clinical viral isolates was 12 nM (St. Clair MH, Millard J, Rooney J, Tisdale M, Parry N, Sadler BM, Blum MR, Painter G (1996) Antiviral Res. 29:53-56). HIV-1 variants 100-fold resistant to amprenavir have been selected by in vitro passage experiments (id). DNA sequence analysis of the protease of these variants revealed a sequential accumulation of point mutations resulting in amino acid substitutions L10F, M46I, I47V, and I50V. The key resistance mutation in the HIV-1 protease substrate binding site is I50V. As a single mutation it confers a two- to threefold decrease in susceptibility (ibid). The other substitutions did not result in reduced susceptibility when introduced as single mutations into an HIV-1 infectious clone (HXB2). However, a triple protease mutant clone containing the mutations M46I, I47V, and I50V was 20-fold less susceptible to amprenavir than wild-type virus. The I50V mutation has not been frequently reported in resistance studies with other HIV protease inhibitors. Kinetic characterization of these substitutions demonstrated an 80-fold reduction in the inhibition constant (K_i) for the I50V single-mutant protease and a 270-fold-reduced K_i for the triple mutant M46I/I47V/I50V, compared to the wild-type enzyme

(Pazhanisamy S, St6uvr CM, Cullinan AB, Margolin N, Rao BG (1996) J. Biol. Chem. 271:17979-17985). The single mutants L10F, M46I, and I47V did not display reduced affinity for amprenavir. The catalytic efficiency (k_{cat}/K_m) of the I50V mutant was decreased up to 25-fold, while the triple mutant M46I/I47V/I50V had a 2-fold-higher processing efficiency than the I50V single mutant, confirming the compensatory role of the M46I-and-I47V mutation. The reduced catalytic efficiency (k_{cat}/K_m) for these mutants in processing peptides appeared to be due to both increased K_m and decreased k_{cat} values.

VIRAL FITNESS

The relative ability of a given virus or virus mutant to replicate is termed viral fitness. Fitness is dependent on both viral and host factors, including the genetic composition of the virus, the host immune response, and selective pressures such as the presence of anti-viral compounds. Many drug-resistant variants of HIV-1 are less fit than the wild-type, i.e. they grow more slowly in the absence of drug selection. However, since the replication of the wild-type virus is inhibited in the presence of drug, the resistant mutant can outgrow it. The reduction in fitness may be a result of several factors including: decreased ability of the mutated enzyme (i.e. PR or RT) to recognize its natural substrates, decreased stability of the mutant protein, or decreased kinetics of enzymatic catalysis. See Back et al., EMBO J. 15: 4040-4049, 1996; Goudsmit et al., J. Virol. 70: 5662-5664, 1996; Maschera et al., J. Biol. Chem. 271: 33231-33235, 1996; Croteau et al., J. Virol. 71: 1089-1096, 1997; Zennou et al., J. Virol. 72: 300-3306, 1998; Harrigan et al., J. Virol. 72:

3773-3778, 1998; Kosalaraksa et al., J. Virol. 73:
5356-5363, 1999; Gerondelis et al., J. Virol. 73:
5803-5813, 1999. Drug resistant viruses that are less fit
than wild type may be less virulent i.e. they may cause
5 damage to the host immune system more slowly than a wild
type virus. Immunological decline may be delayed after the
emergence of drug resistant mutants, compared to the rate
of immunological decline in an untreated patient. The
defect causing reductions in fitness may be partially or
10 completely compensated for by the selection of viruses
with additional amino acid substitutions in the same
protein that bears the drug resistance mutations (for
example, see Martinez-Picado et al., J. Virol.
73:3744-3752, 1999), or in other proteins which interact
15 with the mutated enzyme. Thus, amino acids surrounding the
protease cleavage site in the gag protein may be altered
so that the site is better recognized by a drug-resistant
protease enzyme (Doyon et al., J. Virol. 70: 3763-3769,
1996; Zhang et al., J. Virol. 71: 6662-6670, 1997; Mammano
20 et al., J. Virol. 72: 7632-7637, 1998).

INTEGRASE

Integration of viral DNA into the host chromosome is a
necessary process in the HIV replication cycle (Brown,
25 P.O., 1997, in *Retroviruses*; Coffin, J.M., Hughes, S.H. &
Varmus, H.E., eds., Cold Spring Harbor Lab. Press,
Plainview, NY, 161-203). The key steps of DNA integration
are carried out by the viral integrase protein, which,
along with protease and reverse transcriptase, is one of
30 three enzymes encoded by HIV. Combination antiviral
therapy with protease and reverse transcriptase inhibitors
has demonstrated the potential therapeutic efficacy of

antiviral therapy for treatment for AIDS (Vandamme, A.M.,
Van Vaerenbergh, K. & De Clerq, E., 1998, *Antiviral Chem.*
Chemother. 9, 187-203). However, the ability of HIV to
5 rapidly evolve drug resistance, together with toxicity
problems, requires the development of additional classes
of antiviral drugs. Integrase is an attractive target for
antivirals because it is essential for HIV replication
and, unlike protease and reverse transcriptase, there are
no known counterparts in the host cell. Furthermore,
10 integrase uses a single active site to accommodate two
different configurations of DNA substrates, which may
constrain the ability of HIV to develop drug resistance to
integrase inhibitors. However, unlike protease and
reverse transcriptase, for which several classes of
15 inhibitors have been developed and cocrystal structures
have been determined, progress with the development of
integrase inhibitors has been slow. A major obstacle has
been the absence of good [^]lead compounds that can serve [^]as
the starting point for structure-based inhibitor
20 development. Although numerous compounds have been
reported to inhibit integrase activity *in vitro*, most of
these compounds exhibit little specificity for integrase
and are not useful as lead compounds (Pommier, Y., Pilon,
A.A., Bajaj K, K., Mazumder, A. & Neamati, N., 1997,
25 *Antiviral Chem. Chemother* 8).

HIV-1 integrase is a 32-kDa enzyme that carries out DNA
integration in a two-step reaction (Brown, P.O., *ibid.*).
In the first step, called 3' processing, two nucleotides
30 are removed from each 3' end of the viral DNA made by
reverse transcription. In the next step, called DNA
strand transfer, a pair of transesterification reactions

integrates the ends of the viral DNA into the host genome. Integrase is comprised of three structurally and functionally distinct domains, and all three domains are required for each step of the integration reaction

5 (Engelman, A. Bushman, F.D. & Craigie, R., 1993, *EMBO J.* 12, 3269-3275). The isolated domains form homodimers in solution, and the three-dimensional structures of all three separate dimers have been determined (Dyda, F., Hickman, A.B. Jenkins, T.M., Engelman, A., Craigie, R. &

10 Davies, D.R., 1994, *Science* 226, 1981-1986; Goldgur, Y. Dyda, Hickman, A.B., Jenkins, T.M., Craigie, R. & Davies, D.R., 1998, *Proc. Natl. Acad. Sci., USA* 95, 9150-9154; Maignan, S., Guilloteau, J.P., Zhou-Liu, Q., Clement-Mella, C. & Mikol, V., 1998, *J Mol. Biol.* 282, 259-368;

15 Lodi, P.J., Ernst, J.A., Kuszewski, J., Hickman, A.B., Engelman, A., Craigie, R., Clore, G.M. & Gronenborn, A.M. 1995 *Biochemistry* 34, 9826-9833; Eijkelenboom, A.P., Lutzke, R.A., Boelens, R., Plasterk, R.H., Kaptein, R. & Hard, K. 1995 *Nat. Struct. Biol.* 2, 807-810; Cai, M.L.,

20 Zheng, R., Caffrey, M., Craigie, R., Clore, G.M. & Gronenborn, A.M., 1997 *Nat. Struct. Biol.* 4, 839-840). Although little is known concerning the organization of these domains in the active complex with DNA substrates, integrase is likely to function as at least a tetramer

25 (Dyda, F., Hickman, A.B. Jenkins, T.M., Engelman, A., Craigie, R. & Davies, D.R., 1994, *Science* 226, 1981-1986). Extensive mutagenesis studies mapped the catalytic site to the core domain (residues 50-212), which contains the catalytic residues D64, D116, and E152 (Engelman, A. &

30 Craigie R., 1992, *J. Virol.* 66, 6361-6369; Kulkosky, J., Jones, K.S., Katz, R.A., Mack, J.P. & Skalka, A.M., 1992, *Mol. Cell Biol* 12, 2331-2338). The structure of this

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domain of HIV-1 integrase has been determined in several crystal forms (Dyda, F., Hickman, A.B. Jenkins, T.M., Engelman, A., Craigie, R. & Davies, D.R., 1994, *Science* 226, 1981-1986; Goldgur, Y. Dyda, Hickman, A.B., Jenkins, T.M., Craigie, R. & Davies, D.R., 1998, *Proc. Natl. Acad. Sci., USA* 95, 9150-9154; Maignan, S., Guilloteau, J.P., Zhou-Liu, Q., Clement-Mella, C. & Mikol, V., 1998, *J Mol. Biol.* 282, 259-368).

Hazuda et al. (*Science* 287: 646-650, 2000) have described compounds (termed L-731, 988 and L-708,906) which specifically inhibit the strand-transfer activity of HIV-1 integrase and HIV-1 replication in vitro. Viruses grown in the presence of these inhibitors display reduced inhibitor susceptibility and bear mutations in the integrase coding region at amino acid positions 66 (T66I), 153 (S153Y), and 154 (M154I). Site-directed mutants of a laboratory strain of ^ΔHIV-1 (HXB2) with these amino^Δ acid changes confirmed their direct role in conferring reduced integrase inhibitor susceptibility. In addition some of these mutants displayed delayed growth kinetics, suggesting that viral fitness was impaired.

It is an object of this invention to provide a drug susceptibility and resistance test capable of showing whether a viral population in a patient is either more or less susceptible to a given prescribed drug. Another object of this invention is to provide a test that will enable the physician to substitute one or more drugs in a therapeutic regimen for viruses that show altered susceptibility to a given drug or drugs after a course of therapy. Yet another object of this invention is to

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provide a test that will enable selection of an effective drug regimen for the treatment of HIV infections and/or AIDS. Yet another object of this invention is to provide the means for identifying alterations in the drug susceptibility profile of a patient's virus, in particular identifying changes in susceptibility to protease inhibitors. Still another object of this invention is to provide a test and methods for evaluating the biological effectiveness of candidate drug compounds which act on specific viruses, viral genes and/or viral proteins particularly with respect to alterations in viral drug susceptibility associated with protease inhibitors. It is also an object of this invention to provide the means and compositions for evaluating HIV antiretroviral drug resistance and susceptibility.

It is an object of this invention to provide a method for measuring replication fitness which can be adapted to viruses, including, but not limited to human immunodeficiency virus (HIV), hepadnaviruses (human hepatitis B virus), flaviviruses (human hepatitis C virus) and herpesviruses (human cytomegalovirus). This and other objects of this invention will be apparent from the specification as a whole.

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Summary of the Invention

The present invention relates to methods of monitoring, via phenotypic and genotypic methods the clinical progression of human immunodeficiency virus infection and its response to antiviral therapy. The invention is also based, in part, on the discovery that genetic changes in HIV protease (PR) which confer changes in susceptibility to antiretroviral therapy may be rapidly determined directly from patient plasma HIV RNA using phenotypic or genotypic methods. The methods utilize nucleic acid amplification based assays, such as polymerase chain reaction (PCR). Herein—after, such nucleic acid amplification based assays will be referred to as PCR based assays. This invention is based in part on the discovery of mutations at codons 10, 20, 36, 46, 63, 77 and 88 of HIV protease in PRI treated patients in which the presence of certain combinations of these mutations correlate with changes in [^]certain PRI susceptibilities.[^] This invention is also based on the discovery that susceptibility to HIV protease antivirals may not be altered even if primary mutations are present. Additional mutations at secondary positions in HIV protease are required for a reduction in virus susceptibility. This invention established for the first time that a mutation at position 82 of protease (V82A, F, S, or T) in the absence of another primary mutation was not correlated with a reduction in drug susceptibility. Decreased susceptibility to protease inhibitors, such as indinavir and saquinavir, in viruses containing V82A, F, S or T was observed in viruses with additional mutations at secondary positions, such as, 24, 71, 54, 46, 10 and/or 63 as described herein. Decreased susceptibility to protease

inhibitors, such as indinavir and saquinavir, in viruses containing V82A, F, S or T was also observed in viruses with at least 3 or more additional mutations at secondary positions. This inventions also established for the first time that a mutation at position 90 of protease (L90M) in the absence of another primary mutation was not correlated with a reduction in drug susceptibility. Decreased susceptibility to protease inhibitors, such as indinavir and saquinavir, in viruses containing L90M was observed in viruses with additional mutations at secondary positions, such as, 73, 71, 77, and/or 10 as described herein. Decreased susceptibility to protease inhibitors, such as indinavir and saquinavir, in viruses containing L90M was also observed in viruses with at least 3 or more additional mutations at secondary positions. The mutations were found in plasma HIV nucleic acid after a period of time following the initiation of therapy. The development of these[^] mutations, or combinations of[^] these mutations, in HIV PR was found to be an indicator of the development of alterations in phenotypic susceptibility/resistance, which can be associated with virologic failure and subsequent immunological response.

In one embodiment of the invention, a method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient is provided comprising: (a) collecting a plasma sample from the HIV-infected patient; (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at primary and secondary positions; and (c) determining changes in susceptibility to a protease inhibitor.

In a further embodiment of the invention, PCR based assays, including phenotypic and genotypic assays, may be used to detect a substitution at codon 88 from asparagine to a serine residue either alone or in combination with one or more mutations at other codons selected from the group consisting of 10, 20, 36, 46, 63 and/or 77 or a combination thereof of HIV PR. A mutation at codon 88 from an asparagine residue to a serine residue (N88S) alone correlates with an increase in susceptibility to amprenavir and a mutation at codon 88 from an asparagine residue to a serine residue in combination with mutations at codons 63 and/or 77 or a combination thereof correlates with an increase in susceptibility to amprenavir and a decrease in nelfinavir and indinavir susceptibility.

In a further embodiment of the invention, PCR based assays, including phenotypic and genotypic assays, may be used to detect mutations at codons 10, 20, 36, 46, 63, 77, and 88 of HIV PR which correlate with changes in susceptibility to antiretroviral therapy and immunologic response. Once mutations at these loci have been detected in a patient undergoing PRI antiretroviral therapy, an alteration in the therapeutic regimen should be considered. The timing at which a modification of the therapeutic regimen should be made, following the assessment of antiretroviral therapy using PCR based assays, may depend on several factors including the patient's viral load, CD4 count, and prior treatment history.

In a further embodiment of the invention, PCR based assays, including phenotypic and genotypic assays, may be

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used to detect a substitution at codon 82 from valine to an alanine (V82A), phenylalanine (V82F), serine (V82S), or threonine (V82T) residue either alone or in combination with one or more mutations at other codons, referred to herein as secondary mutations, selected from the group consisting of 20, 24, 36, 71, 54, 46, 63 and/or 10 or a combination thereof of HIV PR. A mutation at codon 82 from a valine residue to a alanine, phenylalanine, serine or threonine alone correlates with susceptibility to certain protease inhibitors including indinavir and saquinavir. A mutation at codon 82 from a valine residue to a alanine, phenylalanine, serine or threonine in combination with secondary mutations at codons 24 and/or 71 or 20 and/or 36 correlates with a reduction in susceptibility to indinavir and saquinavir, respectively. A mutation at codon 82 from a valine residue to a alanine, phenylalanine, serine or threonine in combination with at least 3 secondary mutations correlates with a reduction in susceptibility to indinavir and saquinavir.

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In a further embodiment of the invention, PCR based assays, including phenotypic and genotypic assays, may be used to detect a substitution at codon 90 from leucine to a methionine (L90M) residue either alone or in combination with one or more mutations at other codons, referred to herein as secondary mutations, selected from the group consisting of 73, 71, 46 and/or 10 or a combination thereof of HIV PR. A mutation at codon 90 from a leucine residue to a methionine alone correlates with susceptibility to certain protease inhibitors including indinavir and saquinavir. A mutation at codon 90 from a leucine residue to a methionine in combination with

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secondary mutations at codons 73 and/or 71 or 73, 71 and/or 77 correlates with a reduction in susceptibility to indinavir and saquinavir, respectively. A mutation at codon 90 from a leucine residue to a methionine in combination with at least 3 secondary mutations correlates with a reduction in susceptibility to indinavir and saquinavir.

In another aspect of the invention there is provided a method for assessing the effectiveness of a protease inhibitor antiretroviral drug comprising: (a) introducing a resistance test vector comprising a patient-derived segment and an indicator gene into a host cell; (b) culturing the host cell from step (a); (c) measuring expression of the indicator gene in a target host cell wherein expression of the indicator gene is dependent upon the patient derived segment; and (d) comparing the expression of the indicator gene from step (c) with the expression of the indicator gene measured when steps (a) - (c) are carried out in the absence of the PRI anti-HIV drug, wherein a test concentration of the PRI, anti-HIV drug is presented at steps (a) - (c); at steps (b) - (c); or at step (c).

This invention also provides a method for assessing the effectiveness of protease inhibitor antiretroviral therapy in a patient comprising: (a) developing a standard curve of drug susceptibility for an PRI anti-HIV drug; (b) determining PRI anti-HIV drug susceptibility in the patient using the susceptibility test described above; and (c) comparing the PRI anti-HIV drug susceptibility in step (b) with the standard curve determined in step (a), wherein a decrease in PRI anti-HIV susceptibility

indicates development of anti-HIV drug resistance in the patient's virus and an increase in PRI anti-HIV susceptibility indicates drug hypersensitivity in the patient's virus.

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This invention also provides a method for evaluating the biological effectiveness of a candidate PRI HIV antiretroviral drug compound comprising: (a) introducing a resistance test vector comprising a patient-derived segment and an indicator gene into a host cell; (b) culturing the host cell from step (a); (c) measuring expression of the indicator gene in a target host cell wherein expression of the indicator gene is dependent upon the patient derived segment; and (d) comparing the expression of the indicator gene from step (c) with the expression of the indicator gene measured when steps (a) - (c) are carried out in the absence of the candidate PRI anti-viral drug compound, wherein a test concentration of the candidate PRI anti-viral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

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The expression of the indicator gene in the resistance test vector in the target cell is ultimately dependent upon the action of the HIV enzymes (PR and RT) encoded by the patient-derived segment DNA sequences. The indicator gene may be functional or non-functional.

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In another aspect this invention is directed to antiretroviral drug susceptibility and resistance tests for HIV/AIDS. Particular resistance test vectors of the invention for use in the HIV/AIDS antiretroviral drug susceptibility and resistance test are identified.

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Yet another aspect of this invention provides for the identification and assessment of the biological effectiveness of potential therapeutic antiretroviral compounds for the treatment of HIV and/or AIDS. In another aspect, the invention is directed to a novel resistance test vector comprising a patient-derived segment further comprising one or more mutations on the PR gene and an indicator gene.

Still another aspect of this invention provides for the identification and assessment of the fitness of a virus infecting a patient. In another aspect, the invention is directed to a novel resistance test vector comprising a patient-derived segment further comprising one or more mutations on the PR gene and an indicator gene, enabling the measurement of viral fitness.

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Brief Description of the Drawings

Fig. 1

Resistance Test Vector. A diagrammatic representation of the resistance test vector comprising a patient derived segment and an indicator gene.

Fig. 2

Two Cell Assay. Schematic Representation of the Assay. A resistance test vector is generated by cloning the patient-derived segment into an indicator gene viral vector. The resistance test vector is then co-transfected with an expression vector that produces amphotropic murine leukemia virus (MLV) envelope protein or other viral or cellular proteins which enable infection. Pseudotyped viral particles are produced containing the protease (PR) and the reverse transcriptase (RT) gene products encoded by the patient-derived DNA sequences. The particles are then harvested and used to infect fresh cells. Using defective PR and RT sequences it was shown that luciferase activity is dependent on functional PR and RT. PR inhibitors are added to the cells following transfection and are thus present during particle maturation. RT inhibitors, on the other hand, are added to the cells at the time of or prior to viral particle infection. The assay is performed in the absence of drug and in the presence of drug over a wide range of concentrations. Luciferase activity is determined and the percentage (%) inhibition is calculated at the different drug concentrations tested.

Fig. 3

Sub. B2

Examples of phenotypic drug susceptibility profiles. Data are analyzed by plotting the percent inhibition of luciferase activity vs. log10 concentration. This plot is used to calculate the drug concentration that is required to inhibit virus replication by 50% (IC50) or by 95% (IC95). Shifts in the inhibition curves towards higher drug concentrations are interpreted as evidence of drug resistance. Three typical curves for a nucleoside reverse transcriptase inhibitor (AZT), a non-nucleoside reverse transcriptase inhibitor (efavirenz), and a protease inhibitor (indinavir) are shown. A reduction in drug susceptibility (resistance) is reflected in a shift in the drug susceptibility curve toward higher drug concentrations (to the right) as compared to a baseline (pre-treatment) sample or a drug susceptible virus reference control, such as pNL4-3 or HXB-2, when a baseline sample is not available.

Fig. 4

Sub. B3

Phenotypic PRI susceptibility profile: patient 0732. A PCR-based phenotypic susceptibility assay was carried out giving the phenotypic drug susceptibility profile showing decreased susceptibility to nelfinavir and indinavir, and increased susceptibility to amprenavir.

Fig. 5

Sub. B4

Phenotypic PRI susceptibility profile of a protease mutant generated by site-specific oligonucleotide-directed mutagenesis. A PCR-based phenotypic susceptibility assay was carried out giving the phenotypic drug susceptibility profile of a virus having substitutions at codons 63, 77

Sub. B4
~~and 88 (L63P, V77I and N88S). The profile demonstrates resistance to both nelfinavir and indinavir, and increased susceptibility to amprenavir.~~

5 Figure 6. Distribution of saquinavir hyper-susceptibility by amino acid change at position 82.

Figure 7. Relative luciferase activity of integrase inhibitor-resistant site-directed mutants.

10

Fig. A

Two Cell Fitness Assay. Schematic Representation of the Fitness Assay. A fitness test vector is generated by cloning the patient-derived segment into an indicator gene viral vector. The fitness test vector is then co-transfected with an expression vector that produces amphotropic murine leukemia virus (MLV) envelope protein or other viral or cellular proteins which enable infection. Pseudotyped viral particles are produced containing the protease (PR) and the reverse transcriptase (RT) gene products encoded by the patient-derived DNA sequences. The particles are then harvested and used to infect fresh cells. Using defective PR and RT sequences it was shown that luciferase activity is dependent on functional PR and RT. The fitness assay is typically performed in the absence of drug. If desired, the assay can also be performed at defined drug concentrations. Luciferase activity produced by patient derived viruses is compared to the luciferase activity produced by well-characterized reference viruses. Replication fitness is expressed as a percent of the reference.

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Figure B.

Determining the replication fitness of patient viruses. Virus stocks produced from fitness test vectors derived from patient samples were used to infect cells. Luciferase activity was measured at various times after infection. Patient derived viruses may produce more, approximately the same, or less luciferase activity than the reference virus (Ref) and are said to have greater, equivalent, or reduced replication fitness, respectively. The drug susceptibility profiles of three representative patient derived viruses are shown (P1, P2, P3).

Figure C.

Identifying alterations in protease or reverse transcriptase function associated with differences in replication fitness of patient viruses. Replication fitness is expressed as a percent of the reference virus (top). Fitness measurements are compared to protease processing of the p55 gag polyprotein (middle) and reverse transcriptase activity (bottom). Protease processing is measured by Western blot analysis using an antibody that reacts with the mature capsid protein (p24). The detection of unprocessed p55 or incompletely processed p41 polyproteins are indicators of reduced cleavage. Reverse transcriptase activity is measured using a quantitative RT-PCR assay and is expressed as a percent of the reference virus.

Figure D.

Correlating reduced replication fitness with reduced reverse transcriptase activity. Viruses containing

various amino acid substitutions at position 190 (A, S, C, Q, E, T, V) of reverse transcriptase were constructed using site directed mutagenesis. The reference virus contains G at this position. Replication fitness and

5

reverse transcriptase activities were compared.

Figure E.

Correlating reduced replication fitness with reduced protease processing of p55 gag. Viruses containing various amino acid substitutions in protease (D30N, L90M, etc) were constructed using site directed mutagenesis. Replication fitness and p55 gag processing were compared.

10

Figure F.

Correlating reduced replication fitness with reduced drug susceptibility. A large collection (n=134) of patient samples were evaluated for phenotypic drug susceptibility and replication fitness. Replication fitness and drug susceptibility were compared.

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Figure G.

Relationship between protease inhibitor susceptibility and replication fitness. Patient samples were sorted based on their replication fitness (<25% of reference, 26-75% of reference, and >75% of reference). Mean values for protease inhibitor susceptibility were determined for each fitness group and plotted for each drug and all drugs combined.

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Figure H.

Relationship between reverse transcriptase inhibitor

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5 susceptibility and replication fitness. Patient samples were sorted based on their replication fitness (<25% of reference, 26-75% of reference, and >75% of reference). Mean values for reverse transcriptase susceptibility were determined for each fitness group and plotted for each drug and all drugs combined.

Figure I.

10 Reduced replication fitness is associated with high numbers of protease mutations, and the L90M mutation. Patient viruses were sorted based on the number of protease mutations. Viruses with large numbers of protease mutations or the L90M protease mutation generally exhibit reduced replication fitness.

15 Figure J.

Low replication capacity is associated with specific protease mutations.[^] Patient viruses were sorted based on replication capacity. Specific protease mutations either alone (D30N) or in combination (L90M plus others) were observed with high frequency in viruses with reduced replication fitness.

Figure K.

25 Relationship between nelfinavir susceptibility, protease processing and replication fitness. Patient viruses were sorted based on nelfinavir susceptibility (<10 or >10 of reference). Protease processing and replication fitness were plotted for all patient viruses. Viruses with reduced nelfinavir susceptibility generally exhibited reduced protease processing and reduced replication fitness.

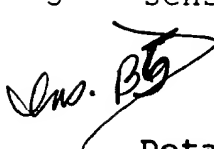
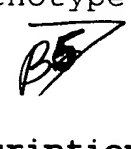
Figure L. Protease mutations associated with reduced protease processing. Patient viruses were sorted based on protease processing. Specific protease mutations were observed at high frequency in viruses with reduced protease processing.

Figure M.
Representative patient sample exhibiting reversion to drug susceptibility during a period of drug treatment interruption. Virus samples were collected weekly during a period of treatment interruption and evaluated for phenotypic drug susceptibility. Values shown represent fold change in susceptibility compared to the reference virus.

Figure N.
Representative patient sample exhibiting increased replication fitness during a period of drug treatment interruption. Virus samples were collected weekly during a period of treatment interruption and evaluated for phenotypic drug susceptibility. Fitness values shown represent percent of the reference virus. The increase in fitness between week 9 and week 10 corresponds to improved protease processing (bottom) and reversion of the drug resistant phenotype to a drug sensitive phenotype (Figure M).

Figure O.
Increased replication fitness during treatment interruption. Replication fitness was measured at the time of treatment interruption and various times during

the period of treatment interruption. Generally, replication fitness was significantly higher in samples that corresponded to timepoints after the virus had reverted from a drug resistant phenotype to a drug sensitive phenotype.

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Detailed Description of the Invention

10 The present invention relates to methods of monitoring the clinical progression of HIV infection in patients receiving antiretroviral therapy, particularly protease inhibitor antiretroviral therapy.

15 In one embodiment, the present invention provides for a method of evaluating the effectiveness of antiretroviral therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; and (ii) determining whether the biological sample comprises
20 nucleic acid encoding HIV PR having a mutation at one or more positions in the PR. The mutation(s) correlate positively with alterations in phenotypic susceptibility.

In a specific embodiment, the invention provides for a
25 method of evaluating the effectiveness of PRI antiretroviral therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; and (ii) determining whether the biological sample comprises nucleic acid encoding HIV PR having a
30 mutation at codon 88 from an asparagine residue to a serine residue (N88S). This invention established, using a phenotypic susceptibility assay, that a mutation at

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codon 88 to a serine residue of HIV protease is correlated with an increase in amprenavir susceptibility.

5 In a specific embodiment, the invention provides for a method of evaluating the effectiveness of PRI antiretroviral therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; and (ii) determining whether the biological sample comprises nucleic acid encoding HIV PR having a
10 mutation at codon 88 from an asparagine residue to a serine residue (N88S) either alone or in combination with mutations at codons 63 and/or 77 or a combination thereof. This invention established, using a phenotypic susceptibility assay, that a mutation at codon 88 to a
15 serine residue of HIV protease is correlated with an increase in amprenavir susceptibility and a mutation at codon 88 to a serine residue in combination with mutations at codons 63 and/or 77 or a combination thereof of HIV protease are correlated with an increase in amprenavir
20 susceptibility and a decrease in nelfinavir and indinavir susceptibility.

In a specific embodiment, the invention provides for a method of evaluating the effectiveness of PRI
25 antiretroviral therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; and (ii) determining whether the biological sample comprises nucleic acid encoding HIV PR having a mutation at codon 88 from an asparagine residue to a
30 serine residue (N88S) either alone or in combination with mutations at codons 46, 63 and/or 77 or a combination thereof. This invention established, using a phenotypic

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susceptibility assay, that a mutation at codon 88 to a serine residue of HIV protease is correlated with an increase in amprenavir susceptibility and a mutation at codon 88 to a serine residue in combination with mutations at codons 46, 63 and/or 77 or a combination thereof of HIV protease are correlated with an increase in amprenavir susceptibility and a decrease in nelfinavir and indinavir susceptibility.

In a specific embodiment, the invention provides for a method of evaluating the effectiveness of PRI antiretroviral therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; and (ii) determining whether the biological sample comprises nucleic acid encoding HIV PR having a mutation at codon 88 from an asparagine residue to a serine residue (N88S) either alone or in combination with mutations at codons 10, 20, 36, 46, 63 and/or 77 or a combination thereof. This invention established, using a phenotypic susceptibility assay, that a mutation at codon 88 to a serine residue of HIV protease is correlated with an increase in amprenavir susceptibility and a mutation at codon 88 to a serine residue in combination with mutations at codons 10, 20, 36, 46, 63 and/or 77 or a combination thereof of HIV protease are correlated with an increase in amprenavir susceptibility and a decrease in nelfinavir and indinavir susceptibility.

Under the foregoing circumstances, the phenotypic susceptibility profile and genotypic profile of the HIV virus infecting the patient has been altered reflecting a change in response to the antiretroviral agent. In the

case of PRI antiretroviral therapy, the HIV virus infecting the patient may be resistant to one or more PRIs but hypersensitive to another of the PRIs as described herein. It therefore may be desirable after detecting the mutation(s), to either increase the dosage of the antiretroviral agent, change to another antiretroviral agent, or add one or more additional antiretroviral agents to the patient's therapeutic regimen. For example, if the patient was being treated with nelfinavir when the N88S mutation arose, the patient's therapeutic regimen may desirably be altered by either (i) changing to a different PRI antiretroviral agent, such as saquinavir, ritonavir or amprenavir and stopping nelfinavir treatment; or (ii) increasing the dosage of nelfinavir; or (iii) adding another antiretroviral agent to the patient's therapeutic regimen. The effectiveness of the modification in therapy may be further evaluated by monitoring viral burden such as by HIV RNA copy number. A decrease in HIV RNA copy number correlates positively with the effectiveness of a treatment regimen.

The phrase "correlates positively," as used herein, indicates that a particular result renders a particular conclusion more likely than other conclusions.

When reference is made to a particular codon number, it is understood that the codon number refers to the position of the amino acid that the codon codes for. Therefore a codon referencing a particular number is equivalent to a "postion" referencing a particular number, such as for example, "codon 88" or "position 88".

Another preferred, non-limiting, specific embodiment of the invention is as follows: A method of evaluating the effectiveness of PRI therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; (ii) purifying and converting the viral RNA to cDNA and amplifying HIV sequences using HIV primers that result in a PCR product that comprises the PR gene; (iii) performing PCR using primers that result in PCR products comprising wild type or serine at codon 88; and (iv) determining, via the products of PCR, the presence or absence of a serine residue at codon 88.

Another preferred, non-limiting, specific embodiment of the invention is as follows: A method of evaluating the effectiveness of PRI therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; (ii) purifying and converting the viral RNA to cDNA and amplifying HIV sequences using HIV primers that result in a PCR product that comprises the PR gene; (iii) performing PCR using primers that result in PCR products comprising wild type or serine at codon 88 and mutations at codons 63 and/or 77; and (iv) determining, via the products of PCR, the presence or absence of a serine residue at codon 88 and the presence or absence of mutations at codons 63 and/or 77.

Another preferred, non-limiting, specific embodiment of the invention is as follows: A method of evaluating the effectiveness of PRI therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; (ii) purifying and converting the viral RNA to cDNA and amplifying HIV sequences using HIV primers that

result in a PCR product that comprises the PR gene; (iii) performing PCR using primers that result in PCR products comprising wild type or serine at codon 88 and mutations at codons 63, 77 and/or 46 or a combination thereof; and
5 (iv) determining, via the products of PCR, the presence or absence of a serine residue at codon 88 and the presence or absence of mutations at codons 63, 77 and/or 46 or a combination thereof.

10 Another preferred, non-limiting, specific embodiment of the invention is as follows: A method of evaluating the effectiveness of PRI therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; (ii) purifying and converting the viral RNA to
15 cDNA and amplifying HIV sequences using HIV primers that result in a PCR product that comprises the PR gene; (iii) performing PCR using primers that result in PCR products comprising wild type or serine at codon 88 and mutations at codons 63, 77, 46, 10, 20, and/or 36 or a combination
20 thereof; and (iv) determining, via the products of PCR, the presence or absence of a serine residue at codon 88 and the presence or absence of mutations at codons 63, 77, 46, 10, 20, and/or 36 or a combination thereof.

25 The presence of the mutation at codon 88 to a serine of HIV PR indicates that the effectiveness of the current or prospective PRI therapy may require alteration, since as shown by this invention mutation at codon 88 to a serine residue increases the susceptibility to amprenavir. Using
30 the methods of this invention, changes in the PRI therapy would be indicated.

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The presence of the mutation at codon 88 to a serine of alone or in combination with mutations at condons 63, 77, 46, 10, 20, and/or 36 or a combination thereof of HIV PR indicates that the effectiveness of the current or prospective PRI therapy may require alteration, since as shown by this invention a mutation at codon 88 to a serine residue alone increases the susceptibility to amprenavir and a mutation at codon 88 to a serine residue in combination with mutations at condons 63, 77, 46, 10, 20, and/or 36 or a combination increases the susceptibility to amprenavir but also reduces the susceptibility to nelfinavir and indinavir. Using the methods of this invention, changes in the PRI therapy would be indicated.

Another preferred, non-limiting, specific embodiment of the invention is as follows: a method of evaluating the effectiveness of antiretroviral therapy of an HIV-infected patient comprising: (a) collecting a biological sample from an HIV-infected patient; and (b) determining whether the biological sample comprises nucleic acid encoding HIV protease having a mutation at codon 88 to serine. Using the phenotypic susceptibility assay, it was observed that the presence of the mutation at codon 88 to serine of HIV PR causes a an increase in amprenavir susceptibility.

Another preferred, non-limiting, specific embodiment of the invention is as follows: a method of evaluating the effectiveness of antiretroviral therapy of an HIV-infected patient comprising: (a) collecting a biological sample from an HIV-infected patient; and (b) determining whether the biological sample comprises nucleic acid encoding HIV protease having a mutation at codon 88 to serine and

additional mutation(s) at codons 63 and/or 77 or a combination thereof. Using the phenotypic susceptibility assay, it was observed that the presence of the mutation at codon 88 to serine of HIV PR causes an increase in amprenavir susceptibility and the presence of the mutations at codon 88 to serine in combination with a mutation at codon(s) 63 and/or 77 or a combination thereof of HIV PR causes a decrease in nelfinavir and indinavir susceptibility while increasing amprenavir susceptibility.

Another preferred, non-limiting, specific embodiment of the invention is as follows: a method of evaluating the effectiveness of antiretroviral therapy of an HIV-infected patient comprising: (a) collecting a biological sample from an HIV-infected patient; and (b) determining whether the biological sample comprises nucleic acid encoding HIV protease having a mutation at codon 88 to serine and additional mutation(s) at codons 63, 77 and/or 46 or a combination thereof. Using the phenotypic susceptibility assay, it was observed that the presence of the mutation at codon 88 to serine of HIV PR causes an increase in amprenavir susceptibility and the presence of the mutations at codon 88 to serine in combination with a mutation at codon(s) 46, 63 and/or 77 or a combination thereof of HIV PR causes a decrease in nelfinavir and indinavir susceptibility while increasing amprenavir susceptibility.

Another preferred, non-limiting, specific embodiment of the invention is as follows: a method of evaluating the effectiveness of antiretroviral therapy of an HIV-infected patient comprising: (a) collecting a biological sample

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from an HIV-infected patient; and (b) determining whether the biological sample comprises nucleic acid encoding HIV protease having a mutation at codon 88 to serine and additional mutation(s) at codons 63, 77, 46, 10, 20 and/or 36 or a combination thereof. Using the phenotypic susceptibility assay, it was observed that the presence of the mutation at codon 88 to serine of HIV PR causes an increase in amprenavir susceptibility and the presence of the mutations at codon 88 to serine in combination with a mutation at codon(s) 63, 77, 46, 10, 20 and/or 36 or a combination thereof of HIV PR causes a decrease in nelfinavir and indinavir susceptibility while increasing amprenavir susceptibility.

This invention also provides the means and methods to use the resistance test vector comprising an HIV gene and further comprising a PR mutation for drug screening. More particularly, the invention describes the resistance test vector comprising the HIV protease having a mutation at codon 88 to a serine alone or in combination with mutations at codons 10, 20, 36, 46, 63 and/or 77 or a combination thereof for drug screening. The invention further relates to novel vectors, host cells and compositions for isolation and identification of the HIV-1 protease inhibitor resistant mutant and using such vectors, host cells and compositions to carry out anti-viral drug screening. This invention also relates to the screening of candidate drugs for their capacity to inhibit said mutant.

This invention provides a method for identifying a compound which is capable of affecting the function of the

protease of HIV-1 comprising contacting the compound with the polypeptide(s) comprising all or part of the HIV-1 protease, wherein codon 88 is changed to a serine residue, wherein a positive binding indicates that the compound is capable of affecting the function of said protease.

This invention also provides a method for assessing the viral fitness of patient's virus comprising: (a) determining the luciferase activity in the absence of drug for the reference control using the susceptibility test described above; (b) determining the luciferase activity in the absence of drug for the patient virus sample using the susceptibility test described above; and (c) comparing the luciferase activity determined in step (b) with the luciferase activity determined in step (a), wherein a decrease in luciferase activity indicates a reduction in viral fitness of the patient's virus.

If a resistance test vector is constructed using a patient derived segment from a patient virus which is unfit, and the fitness defect is due to genetic alterations in the patient derived segment, then the virus produced from cells transfected with the resistance test vector will produce luciferase more slowly. This defect will be manifested as reduced luciferase activity (in the absence of drug) compared to the drug sensitive reference control, and may be expressed as a percentage of the control.

In a further embodiment of the invention, PCR based assays, including phenotypic and genotypic assays, may be used to detect mutations at positions 20 and 88 of HIV PR, which correlate with a reduction in viral fitness and

immunological response.

It is a further embodiment of this invention to provide a means and method for measuring replication fitness for viruses, including, but not limited to human immunodeficiency virus (HIV), hepadnaviruses (human hepatitis B virus), flaviviruses (human hepatitis C virus) and herpesviruses (human cytomegalovirus).

This invention further relates to a means and method for measuring the replication fitness of HIV-1 that exhibits reduced drug susceptibility to reverse transcriptase inhibitors and protease inhibitors.

In a further embodiment of the invention, a means and methods are provided for measuring replication fitness for other classes of inhibitors of HIV-1 replication, including, but not limited to integration, virus assembly, and virus attachment and entry.

This invention relates to a means and method for identifying mutations in protease or reverse transcriptase that alter replication fitness.

In a further embodiment of the invention, a means and methods are provided for identifying mutations that alter replication fitness for other components of HIV-1 replication, including, but not limited to integration, virus assembly, and virus attachment and entry.

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This invention also relates to a means and method for quantifying the affect that specific mutations in protease or reverse transcriptase have on replication fitness.

5 In a further embodiment of the invention , a means and method are provided for quantifying the affect that specific protease and reverse transcriptase mutations have on replication fitness in other viral genes involved in HIV-1 replication, including, but not limited to the gag, 10 pol, and envelope genes.

This invention also relates to the high incidence of patient samples with reduced replication fitness.

15 This invention relates to the correlation between reduced drug susceptibility and reduced replication fitness.

This invention\ further relates to the occurrence of viruses with reduced fitness in patients receiving 20 protease inhibitor and/or reverse transcriptase inhibitor treatment.

This invention further relates to the incidence of patient samples with reduced replication fitness in which the 25 reduction in fitness is due to altered protease processing of the gag polyprotein (p55).

This invention further relates to the incidence of protease mutations in patient samples that exhibit low, 30 moderate or normal (wildtype) replication fitness.

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This invention further relates to protease mutations that are frequently observed, either alone or in combination, in viruses that exhibit reduced replication capacity.

5 This invention also relates to the incidence of patient samples with reduced replication fitness in which the reduction in fitness is due to altered reverse transcriptase activity. This invention relates to the occurrence of viruses with reduced replication fitness in
10 patients failing antiretroviral drug treatment. This invention further relates to a means and method for using replication fitness measurements to guide the treatment of HIV-1. This invention further relates to a means and method for using replication fitness measurements to guide
15 the treatment of patients failing antiretroviral drug treatment. This invention further relates to the means and methods for using replication fitness measurements to guide the treatment of patients newly infected with HIV-1.

20 This invention, provides the means and methods for using replication fitness measurements to guide the treatment of viral diseases, including, but not limited to HIV-1, hepadnaviruses (human hepatitis B virus), flaviviruses (human hepatitis C virus) and herpesviruses (human
25 cytomegalovirus).

In a further embodiment, the invention provides a method for determining replication capacity for a patient's virus comprising:

30

- (a) introducing a resistance test vector comprising a patient derived segment and an indicator gene into a host cell;

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(b) culturing the host cell from (a);

(c) harvesting viral particles from step (b) and infecting target host cells;

5

(d) measuring expression of the indicator gene in the target host cell, wherein the expression of the indicator gene is dependent upon the patient-derived segment;

10

(e) comparing the expression of the indicator gene from (d) with the expression of the indicator gene measured when steps (a) through (d) are carried out in a control resistance test vector; and

15

(f) normalizing the expression of the indicator gene by measuring an amount of virus in step (c).

20 As used herein, "patient-derived segment" encompasses segments derived from human and various animal species. Such species include, but are not limited to chimpanzees, horses, cattles, cats and dogs.

25 Patient-derived segments can also be incorporated into resistance test vectors using any of several alternative cloning techniques as set forth in detail in US Patent Number 5,837,464 (International Publication Number WO 97/27319) which is hereby incorporated by reference. For
30 example, cloning via the introduction of class II restriction sites into both the plasmid backbone and the patient-derived segments or by uracil DNA glycosylase primer cloning.

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The patient-derived segment may be obtained by any method of molecular cloning or gene amplification, or modifications thereof, by introducing patient sequence acceptor sites, as described below, at the ends of the patient-derived segment to be introduced into the resistance test vector. For example, in a gene amplification method such as PCR, restriction sites corresponding to the patient-sequence acceptor sites can be incorporated at the ends of the primers used in the PCR reaction. Similarly, in a molecular cloning method such as cDNA cloning, said restriction sites can be incorporated at the ends of the primers used for first or second strand cDNA synthesis, or in a method such as primer-repair of DNA, whether cloned or uncloned DNA, said restriction sites can be incorporated into the primers used for the repair reaction. The patient sequence acceptor sites and primers are designed to improve the representation of patient-derived segments. Sets of resistance test vectors having designed patient sequence acceptor sites provide representation of patient-derived segments that may be underrepresented in one resistance test vector alone.

"Resistance test vector" means one or more vectors which taken together contain DNA comprising a patient-derived segment and an indicator gene. Resistance test vectors are prepared as described in US Patent Number 5,837,464 (International Publication Number WO 97/27319), which is hereby incorporated by reference, by introducing patient sequence acceptor sites, amplifying or cloning patient-derived segments and inserting the amplified or cloned sequences precisely into indicator gene viral

vectors at the patient sequence acceptor sites. Alternatively, a resistance test vector (also referred to as a resistance test vector system) is prepared by introducing patient sequence acceptor sites into a packaging vector, amplifying or cloning patient-derived segments and inserting the amplified or cloned sequences precisely into the packaging vector at the patient sequence acceptor sites and co-transfecting this packaging vector with an indicator gene viral vector.

"Indicator or indicator gene," as described in US Patent Number 5,837,464 (International Publication Number WO 97/27319) refers to a nucleic acid encoding a protein, DNA or RNA structure that either directly or through a reaction gives rise to a measurable or noticeable aspect, e.g. a color or light of a measurable wavelength or in the case of DNA or RNA used as an indicator a change or generation of a specific DNA or RNA structure. Preferred examples of an indicator gene is the E. coli lacZ gene which encodes beta-galactosidase, the luc gene which encodes luciferase either from, for example, Photinus pyralis (the firefly) or Renilla reniformis (the sea pansy), the E. coli phoA gene which encodes alkaline phosphatase, green fluorescent protein and the bacterial CAT gene which encodes chloramphenicol acetyltransferase. The indicator or indicator gene may be functional or non-functional as described in US Patent Number 5,837,464 (International Publication Number WO 97/27319).

The phenotypic drug susceptibility and resistance tests of this invention may be carried out in one or more host cells as described in US Patent Number 5,837,464

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(International Publication Number WO 97/27319) which is incorporated herein by reference. Viral drug susceptibility is determined as the concentration of the anti-viral agent at which a given percentage of indicator gene expression is inhibited (e.g. the IC50 for an anti-viral agent is the concentration at which 50% of indicator gene expression is inhibited). A standard curve for drug susceptibility of a given anti-viral drug can be developed for a viral segment that is either a standard laboratory viral segment or from a drug-naive patient (i.e. a patient who has not received any anti-viral drug) using the method described in the aforementioned patent. Correspondingly, viral drug resistance is a decrease in viral drug susceptibility for a given patient compared to such a given standard or when making one or more sequential measurements in the same patient over time, as determined by decreased susceptibility in virus from later time points compared to that from earlier time points.

The antiviral drugs being added to the test system are added at selected times depending upon the target of the antiviral drug. For example, in the case of HIV protease inhibitors, including saquinavir, ritonavir, indinavir, nelfinavir and amprenavir, they are added to packaging host cells at the time of or shortly after their transfection with a resistance test vector, at an appropriate range of concentrations. HIV reverse transcriptase inhibitors, including AZT, ddI, ddC, d4T, 3TC, abacavir, nevirapine, delavirdine and efavirenz are added to target host cells at the time of or prior to infection by the resistance test vector viral particles, at an appropriate range of concentration. Alternatively,

the antiviral drugs may be present throughout the assay. The test concentration is selected from a range of concentrations which is typically between about $8 \times 10^{-6} \mu\text{M}$ and about 2mM and more specifically for each of the following drugs: saquinavir, indinavir, nelfinavir and amprenavir, from about $2.3 \times 10^{-5} \mu\text{M}$ to about $1.5 \mu\text{M}$ and ritonavir, from about $4.5 \times 10^{-5} \mu\text{M}$ to about $3 \mu\text{M}$.

In another embodiment of this invention, a candidate PRI antiretroviral compound is tested in the phenotypic drug susceptibility and resistance test using the resistance test vector comprising PR having a mutation at codon 88 to a serine. The candidate antiviral compound is added to the test system at an appropriate range of concentrations and at the transfection step. Alternatively, more than one candidate antiviral compound may be tested or a candidate antiviral compound may be tested in combination with an approved antiviral drug such as AZT, ddI, ddC, d4T, 3TC, abacavir, delavirdine, nevirapine, efavirenz, saquinavir, ritonavir, indinavir, nelfinavir, amprenavir, or a compound which is undergoing clinical trials such as adefovir and ABT-378. The effectiveness of the candidate antiviral will be evaluated by measuring the expression or inhibition of the indicator gene. In another aspect of this embodiment, the drug susceptibility and resistance test may be used to screen for viral mutants. Following the identification of mutants resistant to either known antiretrovirals or candidate antiretrovirals the resistant mutants are isolated and the DNA is analyzed. A library of viral resistant mutants can thus be assembled enabling the screening of candidate PRI antiretrovirals, alone or in combination. This will enable one of ordinary skill to

identify effective PRI antiretrovirals and design effective therapeutic regimens.

5 In another embodiment of this invention, a method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient is provided comprising:
(a) collecting a biological sample from the HIV-infected patient;
(b) evaluating whether the biological sample contains
10 nucleic acid encoding HIV protease having a mutation at codon 82 or codon 90; and
(c) determining changes in susceptibility to protease inhibitors.

15 In another embodiment of this invention, the method is provided, wherein step (c) determines changes in susceptibility to saquinavir.

20 In another embodiment of this invention, the method is provided , wherein the mutation at codon 82 codes for alanine (A), phenylalanine (F), serine (S), or threonine (T) .

25 In another embodiment of this invention, the method is provided , wherein the mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine(V) .

30 In another embodiment of this invention, the method is provided, wherein the mutation at codon 90 codes for methionine (M) .

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In another embodiment of this invention, the method is provided , wherein the mutation at codon 90 is a substitution of methionine (M) for leucine (L).

5 In another embodiment of this invention, a method for evaluating the biological effectiveness of a candidate HIV protease antiretroviral drug compound is provided comprising:

10 (a) introducing a resistance test vector comprising a patient-derived segment having nucleic acid encoding HIV protease with a mutation at codon 82 or codon 90 and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

15 (c) measuring the indicator gene in a target host cell; and

(d) comparing the measurement of the indicator gene from step (c) with the measurement of the indicator gene measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

20 wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

25 In another embodiment of this invention, a resistance test vector comprising an HIV patient-derived segment further comprising protease having a mutation at codon 82 or codon 90 and an indicator gene, wherein the expression of the indicator gene is dependent upon the patient-derived segment.

30

In another embodiment of this invention, the resistance test vector is provided , wherein the patient-derived

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segment having a mutation at codon 82 codes for alanine (A), phenylalanine (F), serine (S), or threonine (T).

5 In another embodiment of this invention, the resistance test vector of is provided , wherein the patient-derived segment having a mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine(V).

10 In another embodiment of this invention, the resistance test vector is provided , wherein the patient-derived segment having a mutation at codon 90 codes for methionine (M) .

15 In yet another embodiment of this invention, the resistance test vector is provided, wherein the patient-derived segment having a mutation at codon 90 is a substitution of methionine (M) for leucine (L). ^

20 In another embodiment of this invention, a method for determining replication capacity for a patient's virus is provided comprising:

25 (a)introducing a resistance test vector comprising a patient-derived segment and an indicator gene into a host cell;

(b) culturing the host cell from (a);

(c) harvesting viral particles from step (b) and infecting target host cells;

30 (d) measuring expression of the indicator gene in the target host cell, wherein the expression of the indicator gene is dependent upon the patient-derived segment; and

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(e) comparing the expression of the indicator gene from (d) with the expression of the indicator gene measured when steps (a) through (d) are carried out in a control resistance test vector.

5

In another embodiment of this invention, the method further comprises the step of:

(f) normalizing the expression of the indicator gene by measuring an amount of virus in step (c).

10

In another embodiment of this invention, the method is provided wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having a mutation at codon 66.

15

In another embodiment of this invention, the method is provided wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having a mutation at codon 154.

20

In another embodiment of this invention, the method is provided wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having mutations at codon 66 and codon 153.

25

In another embodiment of this invention, the method is provided wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having mutations at codon 66 and codon 154.

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In another embodiment of this invention, a method is provided of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

- (a) collecting a biological sample from the HIV-infected patient;
- (b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, 90, 13, 84, 23, 33, 74, 32, 39, 60, 36, and 35, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 95, 54, 84, 82, 46, 13, 74, 55, 85, 20, 72, 62, 66, 84, 48, 33, 73, 71, 64, 93, 23, 58, and 36; and
- (c) determining a change in susceptibility to a protease inhibitor.

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, wherein the mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V) and the mutation at codon 90 is a substitution of methionine (M) for leucine (L).

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, wherein the protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir.

5 The structure, life cycle and genetic elements of the
viruses which could be tested in the drug susceptibility
and resistance test of this invention would be known to
one of ordinary skill in the art. It is useful to the
practice of this invention, for example, to understand the
10 life cycle of a retrovirus, as well as the viral genes
required for retrovirus rescue and infectivity.
Retrovirally infected cells shed a membrane virus
containing a diploid RNA genome. The virus, studded with
an envelope glycoprotein (which serves to determine the
15 host range of infectivity), attaches to a cellular
receptor in the plasma membrane of the cell to be
infected. After receptor binding, the virus is
internalized and uncoated as it passes through the
cytoplasm of the host cell. Either on its way to the
20 nucleus or in the nucleus, the reverse transcriptase
molecules resident in the viral core drive the synthesis
of the double-stranded DNA provirus, a synthesis that is
primed by the binding of a tRNA molecule to the genomic
viral RNA. The double-stranded DNA provirus is
25 subsequently integrated in the genome of the host cell,
where it can serve as a transcriptional template for both
mRNAs encoding viral proteins and virion genomic RNA,
which will be packaged into viral core particles. On
their way out of the infected cell, core particles move
30 through the cytoplasm, attach to the inside of the plasma
membrane of the newly infected cell, and bud, taking with
them tracts of membrane containing the virally encoded
envelope glycoprotein gene product. This cycle of
infection - reverse transcription, transcription,
35 translation, virion assembly, and budding - repeats itself

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5 over and over again as infection spreads.

10 The viral RNA and, as a result, the proviral DNA encode several cis-acting elements that are vital to the successful completion of the viral lifecycle. The virion RNA carries the viral promoter at its 3' end. Replicative acrobatics place the viral promoter at the 5' end of the proviral genome as the genome is reverse transcribed. Just 3' to the 5' retroviral LTR lies the viral packaging site. The retroviral lifecycle requires the presence of virally encoded transacting factors. The viral-RNA-dependent DNA polymerase (*pol*)-reverse transcriptase is also contained within the viral core and is vital to the viral life cycle in that it is responsible for the conversion of the genomic RNA to the integrative intermediate proviral DNA. The viral envelope glycoprotein, *env*, is required for viral attachment to the uninfected cell and for viral spread. There are also transcriptional *trans*-activating factors, so called transactivators, that can serve to modulate the level of transcription of the integrated parental provirus. Typically, replication-competent (non-defective) viruses are self-contained in that they encode all of these trans-acting factors. Their defective counterparts are not self-contained.

30

In the case of a DNA virus, such as a hepadnavirus, understanding the life cycle and viral genes required for infection is useful to the practice of this invention. The process of HBV entry has not been well defined. Replication of HBV uses an RNA intermediate template. In the infected cell the first step in replication is the

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5 conversion of the asymmetric relaxed circle DNA (rc-DNA)
to covalently closed circle DNA (cccDNA). This process,
which occurs within the nucleus of infected liver cells,
involves completion of the DNA positive-strand synthesis
and ligation of the DNA ends. In the second step, the
10 cccDNA is transcribed by the host RNA polymerase to
generate a 3.5 kB RNA template (the pregenome). This
pregenome is complexed with protein in the viral core.
The third step involves the synthesis of the first
negative-sense DNA strand by copying the pregenomic RNA
15 using the virally encoded P protein reverse transcriptase.
The P protein also serves as the minus strand DNA primer.
Finally, the synthesis of the second positive-sense DNA
strand occurs by copying the first DNA strand, using the P
protein DNA polymerase activity and an oligomer of viral
20 RNA as primer. The pregenome also transcribes mRNA for
the major structural core proteins.

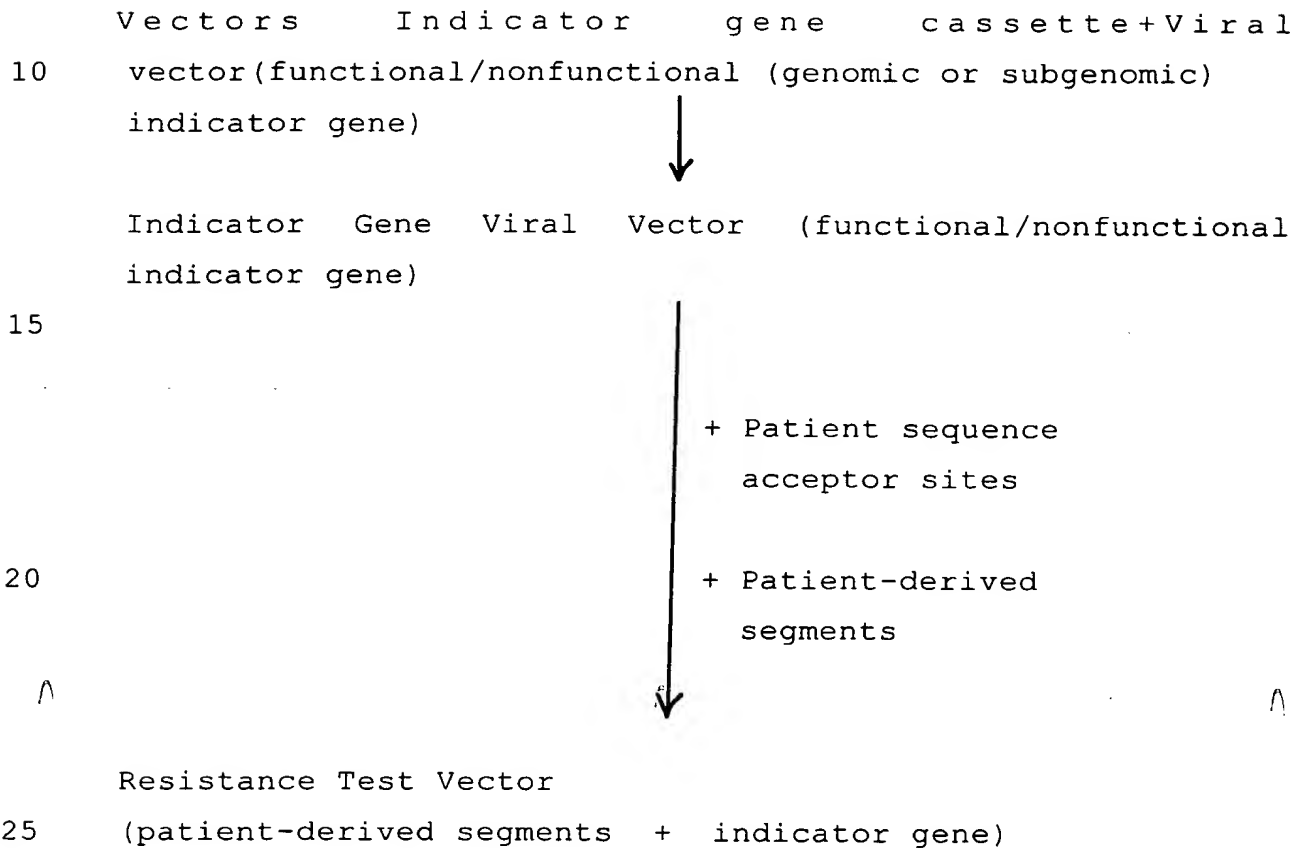
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5 The following flow chart illustrates certain of the various vectors and host cells which may be used in this invention. It is not intended to be all inclusive.



Host Cells

30 Packaging Host Cell - transfected with packaging
expression vectors

Resistance Test Vector Host Cell - a packaging host cell
transfected with a resistance test vector

35

Target Host Cell - a host cell to be infected by a

5 resistance test vector viral particle produced by the
resistance test vector host cell

Resistance Test Vector

10 "Resistance test vector" means one or more vectors which
taken together contain DNA or RNA comprising a
patient-derived segment and an indicator gene. In the
case where the resistance test vector comprises more than
one vector the patient-derived segment may be contained in
one vector and the indicator gene in a different vector.
15 Such a resistance test vector comprising more than one
vector is referred to herein as a resistance test vector
system for purposes of clarity but is nevertheless
understood to be a resistance test vector. The DNA or RNA
of a resistance test vector may thus be contained in one
20 or more DNA or RNA molecules. In one embodiment, the
resistance test vector is made by insertion of a
patient-derived segment into an indicator gene viral
vector. In another embodiment, the resistance test vector
is made by insertion of a patient-derived segment into a
25 packaging vector while the indicator gene is contained in
a second vector, for example an indicator gene viral
vector. As used herein, "patient-derived segment" refers
to one or more viral segments obtained directly from a
patient using various means, for example, molecular
30 cloning or polymerase chain reaction (PCR) amplification
of a population of patient-derived segments using viral
DNA or complementary DNA (cDNA) prepared from viral RNA,
present in the cells (e.g. peripheral blood mononuclear
cells, PBMC), serum or other bodily fluids of infected
35 patients. When a viral segment is "obtained directly"
from a patient it is obtained without passage of the virus

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5 through culture, or if the virus is cultured, then by a
minimum number of passages to essentially eliminate the
selection of mutations in culture. The term "viral
segment" refers to any functional viral sequence or viral
gene encoding a gene product (e.g., a protein) that is the
10 target of an anti-viral drug. The term "functional viral
sequence" as used herein refers to any nucleic acid
sequence (DNA or RNA) with functional activity such as
enhancers, promoters, polyadenylation sites, sites of
action of trans-acting factors, such as *tar* and RRE,
15 packaging sequences, integration sequences, or splicing
sequences. If a drug were to target more than one
functional viral sequence or viral gene product then
patient-derived segments corresponding to each said viral
gene would be inserted in the resistance test vector. In
20 the case of combination therapy where two or more
anti-virals targeting two different functional viral
sequences or viral gene products are being evaluated,
patient-derived segments corresponding to each functional
viral sequence or viral gene product would be inserted in
25 the resistance test vector. The patient-derived segments
are inserted into unique restriction sites or specified
locations, called patient sequence acceptor sites, in the
indicator gene viral vector or for example, a packaging
vector depending on the particular construction being used
30 as described herein.

As used herein, "patient-derived segment" encompasses
segments derived from human and various animal species.
Such species include, but are not limited to chimpanzees,
35 horses, cattles, cats and dogs.

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5 Patient-derived segments can also be incorporated into
resistance test vectors using any of several alternative
cloning techniques. For example, cloning via the
introduction of class II restriction sites into both the
10 plasmid backbone and the patient-derived segments or by
uracil DNA glycosylase primer cloning (refs).

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15 The patient-derived segment may be obtained by any method
of molecular cloning or gene amplification, or
modifications thereof, by introducing patient sequence
acceptor sites, as described below, at the ends of the
patient-derived segment to be introduced into the
resistance test vector. For example, in a gene
amplification method such as PCR, restriction sites
corresponding to the patient-sequence acceptor sites can
20 be incorporated at the ends of the primers used in the PCR
reaction. Similarly, in a molecular cloning method such
as cDNA cloning, said restriction sites can be
incorporated at the ends of the primers used for first or
second strand cDNA synthesis, or in a method such as
25 primer-repair of DNA, whether cloned or uncloned DNA, said
restriction sites can be incorporated into the primers
used for the repair reaction. The patient sequence
acceptor sites and primers are designed to improve the
representation of patient-derived segments. Sets of
30 resistance test vectors having designed patient sequence
acceptor sites provide representation of patient-derived
segments that would be underrepresented in one resistance
test vector alone.

35 Resistance test vectors are prepared by modifying an
indicator gene viral vector (described below) by

5 introducing patient sequence acceptor sites, amplifying or
cloning patient-derived segments and inserting the
amplified or cloned sequences precisely into indicator
gene viral vectors at the patient sequence acceptor sites.

10 The resistance test vectors are constructed from
indicator gene viral vectors which are in turn derived
from genomic viral vectors or subgenomic viral vectors and
an indicator gene cassette, each of which is described
below. Resistance test vectors are then introduced into a
host cell. Alternatively, a resistance test vector (also
15 referred to as a resistance test vector system) is
prepared by introducing patient sequence acceptor sites
into a packaging vector, amplifying or cloning
patient-derived segments and inserting the amplified or
cloned sequences precisely into the packaging vector at
20 the patient sequence acceptor sites and co-transfecting
this packaging vector with an indicator gene viral vector.

25 In one preferred embodiment, the resistance test vector
may be introduced into packaging host cells together with
packaging expression vectors, as defined below, to produce
resistance test vector viral particles that are used in
drug resistance and susceptibility tests that are referred
to herein as a "particle-based test." In an alternative
preferred embodiment, the resistance test vector may be
30 introduced into a host cell in the absence of packaging
expression vectors to carry out a drug resistance and
susceptibility test that is referred to herein as a
"non-particle-based test." As used herein a "packaging
expression vector" provides the factors, such as packaging
35 proteins (e.g. structural proteins such as core and
envelope polypeptides), transacting factors, or genes

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5 required by replication-defective retrovirus or
hepadnavirus. In such a situation, a
replication-competent viral genome is enfeebled in a
manner such that it cannot replicate on its own. This
10 means that, although the packaging expression vector can
produce the trans-acting or missing genes required to
rescue a defective viral genome present in a cell
containing the enfeebled genome, the enfeebled genome
cannot rescue itself.

15 ***Indicator or Indicator Gene***

"Indicator or indicator gene" refers to a nucleic acid
encoding a protein, DNA or RNA structure that either
directly or through a reaction gives rise to a measurable
or noticeable aspect, e.g. a color or light of a
20 measurable wavelength or in the case of DNA or RNA used as
an indicator a change or generation of a specific DNA or
RNA structure. Preferred examples of an indicator gene is
the *E. coli lacZ* gene which encodes beta-galactosidase,
the *luc* gene which encodes luciferase either from, for
25 example, *Photinus pyralis* (the firefly) or *Renilla*
reniformis (the sea pansy), the *E. coli phoA* gene which
encodes alkaline phosphatase, green fluorescent protein
and the bacterial CAT gene which encodes chloramphenicol
acetyltransferase. Additional preferred examples of an
30 indicator gene are secreted proteins or cell surface
proteins that are readily measured by assay, such as
radioimmunoassay (RIA), or fluorescent activated cell
sorting (FACS), including, for example, growth factors,
cytokines and cell surface antigens (e.g. growth hormone,
35 Il-2 or CD4, respectively). "Indicator gene" is
understood to also include a selection gene, also referred

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5 to as a selectable marker. Examples of suitable
selectable markers for mammalian cells are dihydrofolate
reductase (DHFR), thymidine kinase, hygromycin, neomycin,
zeocin or *E. coli* gpt. In the case of the foregoing
10 examples of indicator genes, the indicator gene and the
patient-derived segment are discrete, i.e. distinct and
separate genes. In some cases a patient-derived segment
may also be used as an indicator gene. In one such
embodiment in which the patient-derived segment
corresponds to more than one viral gene which is the
15 target of an anti-viral, one of said viral genes may also
serve as the indicator gene. For example, a viral
protease gene may serve as an indicator gene by virtue of
its ability to cleave a chromogenic substrate or its
ability to activate an inactive zymogen which in turn
20 cleaves a chromogenic substrate, giving rise in each case
to a color reaction. In all of the above examples of
indicator genes, the indicator gene may be either
"functional" or "non-functional" but in each case the
expression of the indicator gene in the target cell is
25 ultimately dependent upon the action of the
patient-derived segment.

Functional Indicator Gene

30 In the case of a "functional indicator gene" the indicator
gene may be capable of being expressed in a "packaging
host cell/resistance test vector host cell" as defined
below, independent of the patient-derived segment,
however the functional indicator gene could not be
expressed in the target host cell, as defined below,
35 without the production of functional resistance test
vector particles and their effective infection of the

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5 target host cell. In one embodiment of a functional indicator gene, the indicator gene cassette, comprising control elements and a gene encoding an indicator protein, is inserted into the indicator gene viral vector with the same or opposite transcriptional orientation as the native or foreign enhancer/promoter of the viral vector. One example of a functional indicator gene in the case of HIV or HBV, places the indicator gene and its promoter (a CMV IE enhancer/promoter) in the same or opposite transcriptional orientation as the HIV-LTR or HBV enhancer-promoter, respectively, or the CMV IE enhancer/promoter associated with the viral vector.

Non-Functional Indicator Gene

Alternatively the indicator gene, may be "non-functional" in that the indicator gene is not efficiently expressed in a packaging host cell transfected with the resistance test vector, which is then referred to a resistance test vector host cell, until it is converted into a functional indicator gene through the action of one or more of the patient-derived segment products. An indicator gene is rendered non-functional through genetic manipulation according to this invention.

1. Permuted Promoter In one embodiment an indicator gene is rendered non-functional due to the location of the promoter, in that, although the promoter is in the same transcriptional orientation as the indicator gene, it follows rather than precedes the indicator gene coding sequence. This misplaced promoter is referred to as a "permuted promoter." In addition to the permuted promoter the orientation of the non-functional indicator gene is

5 opposite to that of the native or foreign
promoter/enhancer of the viral vector. Thus the coding
sequence of the non-functional indicator gene can neither
be transcribed by the permuted promoter nor by the viral
promoters. The non-functional indicator gene and its
10 permuted promoter is rendered functional by the action of
one or more of the viral proteins. One example of a
non-functional indicator gene with a permuted promoter in
the case of HIV, places a T7 phage RNA polymerase promoter
(herein referred to as T7 promoter) promoter in the 5' LTR
15 in the same transcriptional orientation as the indicator
gene. The indicator gene cannot be transcribed by the T7
promoter as the indicator gene cassette is positioned
upstream of the T7 promoter. The non-functional indicator
gene in the resistance test vector is converted into a
20 functional indicator gene by reverse transcriptase upon
infection of the target cells, resulting from the
repositioning of the T7 promoter, by copying from the 5'
LTR to the 3' LTR, relative to the indicator gene coding
region. Following the integration of the repaired
25 indicator gene into the target cell chromosome by HIV
integrase, a nuclear T7 RNA polymerase expressed by the
target cell transcribes the indicator gene. One example
of a non-functional indicator gene with a permuted
promoter in the case of HBV, places an enhancer-promoter
30 region downstream or 3' of the indicator gene both having
the same transcriptional orientation. The indicator gene
cannot be transcribed by the enhancer-promoter as the
indicator gene cassette is positioned upstream. The
non-functional indicator gene in the resistance test
35 vector is converted into a functional indicator gene by
reverse transcription and circularization of the HBV

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5 indicator gene viral vector by the repositioning of the
enhancer-promoter upstream relative to the indicator gene
coding region.

10 A permuted promoter may be any eukaryotic or prokaryotic
promoter which can be transcribed in the target host cell.
Preferably the promoter will be small in size to enable
insertion in the viral genome without disturbing viral
replication. More preferably, a promoter that is small in
size and is capable of transcription by a single subunit
15 RNA polymerase introduced into the target host cell, such
as a bacteriophage promoter, will be used. Examples of
such bacteriophage promoters and their cognate RNA
polymerases include those of phages T7, T3 and Sp6. A
nuclear localization sequence (NLS) may be attached to the
20 RNA polymerase to localize expression of the RNA
polymerase to the nucleus where they may be needed to
transcribed the repaired indicator gene. Such an NLS may
be obtained from any nuclear-transported protein such as
the SV40 T antigen. If a phage RNA polymerase is
25 employed, an internal ribosome entry site (IRES) such as
the EMC virus 5' untranslated region (UTR) may be added in
front of the indicator gene, for translation of the
transcripts which are generally uncapped. In the case of
HIV, the permuted promoter itself can be introduced at any
30 position within the 5' LTR that is copied to the 3' LTR
during reverse transcription so long as LTR function is
not disrupted, preferably within the U5 and R portions of
the LTR, and most preferably outside of functionally
important and highly conserved regions of U5 and R. In
35 the case of HBV, the permuted promoter can be placed at
any position that does not disrupt the cis acting elements

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5 that are necessary for HBV DNA replication. Blocking
sequences may be added at the ends of the resistance test
vector should there be inappropriate expression of the
non-functional indicator gene due to transfection
artifacts (DNA concatenation). In the HIV example of the
10 permuted T7 promoter given above, such a blocking sequence
may consist of a T7 transcriptional terminator, positioned
to block readthrough transcription resulting from DNA
concatenation, but not transcription resulting from
repositioning of the permuted T7 promoter from the 5' LTR
15 to the 3' LTR during reverse transcription.

2. Permuted Coding Region In a second embodiment, an
indicator gene is rendered non-functional due to the
relative location of the 5' and 3' coding regions of the
20 indicator gene, in that, the 3' coding region precedes
rather than follows the 5' coding region. This misplaced
coding region is referred to as a "permuted coding
region." The orientation of the non-functional indicator
gene may be the same or opposite to that of the native or
25 foreign promoter/enhancer of the viral vector, as mRNA
coding for a functional indicator gene will be produced in
the event of either orientation. The non-functional
indicator gene and its permuted coding region is rendered
functional by the action of one or more of the
30 patient-derived segment products. A second example of a
non-functional indicator gene with a permuted coding
region in the case of HIV, places a 5' indicator gene
coding region with an associated promoter in the 3' LTR U3
region and a 3' indicator gene coding region in an
35 upstream location of the HIV genome, with each coding
region having the same transcriptional orientation as the

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5 viral LTRs. In both examples, the 5' and 3' coding
regions may also have associated splice donor and acceptor
sequences, respectively, which may be heterologous or
artificial splicing signals. The indicator gene cannot be
functionally transcribed either by the associated promoter
10 or viral promoters, as the permuted coding region prevents
the formation of functionally spliced transcripts. The
non-functional indicator gene in the resistance test
vector is converted into a functional indicator gene by
reverse transcriptase upon infection of the target cells,
15 resulting from the repositioning of the 5' and 3'
indicator gene coding regions relative to one another, by
copying of the 3' LTR to the 5' LTR. Following
transcription by the promoter associated with the 5'
coding region, RNA splicing can join the 5' and 3' coding
20 regions to produce a functional indicator gene product.
One example of a non-functional indicator gene with a
permuted coding region in the case of HBV, places a 3'
indicator gene coding region upstream or 5' of the
enhancer-promoter and the 5' coding region of the
25 indicator gene. The transcriptional orientation of the
indicator gene 5' and 3' coding regions are identical to
one another, and the same as that of the indicator gene
viral vector. However, as the indicator gene 5' and 3'
coding regions are permuted in the resistance test vectors
30 (i.e., the 5' coding region is downstream of the 3' coding
region), no mRNA is transcribed which can be spliced to
generate a functional indicator gene coding region.
Following reverse transcription and circularization of the
indicator gene viral vector, the indicator gene 3' coding
35 region is positioned downstream or 3' to the
enhancer-promoter and 5' coding regions thus permitting

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5 the transcription of mRNA which can be spliced to generate
a functional indicator gene coding region.

3. Inverted Intron In a third embodiment, the indicator
gene is rendered non-functional through use of an
10 "inverted intron," i.e. an intron inserted into the coding
sequence of the indicator gene with a transcriptional
orientation opposite to that of the indicator gene. The
overall transcriptional orientation of the indicator gene
cassette including its own, linked promoter, is opposite
15 to that of the viral control elements, while the
orientation of the artificial intron is the same as the
viral control elements. Transcription of the indicator
gene by its own linked promoter does not lead to the
production of functional transcripts as the inverted
20 intron cannot be spliced in this orientation.
Transcription of the indicator gene by the viral control
elements does, however, lead to the removal of the
inverted intron by RNA splicing, although the indicator
gene is still not functionally expressed as the resulting
25 transcript has an antisense orientation. Following the
reverse transcription of this transcript and integration
of the resultant retroviral DNA, or the circularization of
hepadnavirus DNA, the indicator gene can be functionally
transcribed using its own linked promoter as the inverted
30 intron has been previously removed. In this case, the
indicator gene itself may contain its own functional
promoter with the entire transcriptional unit oriented
opposite to the viral control elements. Thus the
non-functional indicator gene is in the wrong orientation
35 to be transcribed by the viral control elements and it
cannot be functionally transcribed by its own promoter, as

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5 the inverted intron cannot be properly excised by
splicing. However, in the case of a retrovirus and HIV
specifically and hepadnaviruses, and HBV specifically,
transcription by the viral promoters (HIV LTR or HBV
enhancer-promoter) results in the removal of the inverted
10 intron by splicing. As a consequence of reverse
transcription of the resulting spliced transcript and the
integration of the resulting provirus into the host cell
chromosome or circularization of the HBV vector, the
indicator gene can now be functionally transcribed by its
15 own promoter. The inverted intron, consisting of a splice
donor and acceptor site to remove the intron, is
preferably located in the coding region of the indicator
gene in order to disrupt translation of the indicator
gene. The splice donor and acceptor may be any splice
20 donor and acceptor. A preferred splice donor-receptor is
the CMV IE splice donor and the splice acceptor of the
second[^]exon of the human alpha globin[^]gene ("intron A").

Indicator Gene Viral Vector - Construction

25 As used herein, "indicator gene viral vector" refers to a
vector(s) comprising an indicator gene and its control
elements and one or more viral genes. The indicator gene
viral vector is assembled from an indicator gene cassette
and a "viral vector," defined below. The indicator gene
30 viral vector may additionally include an enhancer,
splicing signals, polyadenylation sequences,
transcriptional terminators, or other regulatory
sequences. Additionally the indicator gene viral vector
may be functional or nonfunctional. In the event that the
35 viral segments which are the target of the anti-viral drug
are not included in the indicator gene viral vector they

5 are provided in a second vector. An "indicator gene
cassette" comprises an indicator gene and control
elements. "Viral vector" refers to a vector comprising
some or all of the following: viral genes encoding a gene
product, control sequences, viral packaging sequences, and
10 in the case of a retrovirus, integration sequences. The
viral vector may additionally include one or more viral
segments one or more of which may be the target of an
anti-viral drug. Two examples of a viral vector which
contain viral genes are referred to herein as an "genomic
15 viral vector" and a "subgenomic viral vector." A "genomic
viral vector" is a vector which may comprise a deletion of
a one or more viral genes to render the virus replication
incompetent, but which otherwise preserves the mRNA
expression and processing characteristics of the complete
20 virus. In one embodiment for an HIV drug susceptibility
and resistance test, the genomic viral vector comprises
the HIV *gag-pol*, *vif*, *vpr*, *tat*, *rev*, *vpu*, and *nef* genes
(some, most or all of *env* may be deleted). A "subgenomic
viral vector" refers to a vector comprising the coding
25 region of one or more viral genes which may encode the
proteins that are the target(s) of the anti-viral drug.
In the case of HIV, a preferred embodiment is a subgenomic
viral vector comprising the HIV *gag-pol* gene. In the case
of HBV a preferred embodiment is a subgenomic viral vector
30 comprising the HBV P gene. In the case of HIV, two
examples of proviral clones used for viral vector
construction are: HXB2 (Fisher et al., (1986) *Nature*, **320**,
367-371) and NL4-3, (Adachi et al., (1986) *J. Virol.*, **59**,
284-291). In the case of HBV, a large number of full
35 length genomic sequences have been characterized and could
be used for construction of HBV viral vectors: GenBank

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5 Nos. M54923, M38636, J02203 and X59795. The viral coding
genes may be under the control of a native
enhancer/promoter or a foreign viral or cellular
enhancer/promoter. A preferred embodiment for an HIV drug
susceptibility and resistance test, is to place the
10 genomic or subgenomic viral coding regions under the
control of the native enhancer/promoter of the HIV-LTR U3
region or the CMV immediate-early (IE) enhancer/promoter.
A preferred embodiment for an HBV drug susceptibility and
resistance test, is to place the genomic or subgenomic
15 viral coding regions under the control of the CMV
immediate-early (IE) enhancer/promoter. In the case of an
indicator gene viral vector that contains one or more
viral genes which are the targets or encode proteins which
are the targets of an anti-viral drug(s) then said vector
20 contains the patient sequence acceptor sites. The
patient-derived segments are inserted in the patient
sequence acceptor site in the indicator gene viral vector
which is then referred to as the resistance test vector,
as described above.

25 "Patient sequence acceptor sites" are sites in a vector
for insertion of patient-derived segments and said sites
may be: 1) unique restriction sites introduced by
site-directed mutagenesis into a vector; 2) naturally
30 occurring unique restriction sites in the vector; or 3)
selected sites into which a patient-derived segment may be
inserted using alternative cloning methods (e.g. UDG
cloning). In one embodiment the patient sequence acceptor
site is introduced into the indicator gene viral vector.
35 The patient sequence acceptor sites are preferably located
within or near the coding region of the viral protein

5 which is the target of the anti-viral drug. The viral
sequences used for the introduction of patient sequence
acceptor sites are preferably chosen so that no change, or
a conservative change, is made in the amino acid coding
sequence found at that position. Preferably the patient
10 sequence acceptor sites are located within a relatively
conserved region of the viral genome to facilitate
introduction of the patient-derived segments.
Alternatively, the patient sequence acceptor sites are
located between functionally important genes or regulatory
15 sequences. Patient-sequence acceptor sites may be located
at or near regions in the viral genome that are relatively
conserved to permit priming by the primer used to
introduce the corresponding restriction site into the
patient-derived segment. To improve the representation of
20 patient-derived segments further, such primers may be
designed as degenerate pools to accommodate viral sequence
heterogeneity, or may incorporate residues such as
deoxyinosine (I) which have multiple base-pairing
capabilities. Sets of resistance test vectors having
25 patient sequence acceptor sites that define the same or
overlapping restriction site intervals may be used
together in the drug resistance and susceptibility tests
to provide representation of patient-derived segments that
contain internal restriction sites identical to a given
30 patient sequence acceptor site, and would thus be
underrepresented in either resistance test vector alone.

Host Cells

The resistance test vector is introduced into a host cell.
35 Suitable host cells are mammalian cells. Preferred host
cells are derived from human tissues and cells which are

5 the principle targets of viral infection. In the case of
HIV these include human cells such as human T cells,
monocytes, macrophage, dendritic cells, Langerhans cells,
hematopoeitic stem cells or precursor cells, and other
cells. In the case of HBV, suitable host cells include
10 hepatoma cell lines (HepG2, Huh 7), primary human
hepatocytes, mammalian cells which can be- infected by
pseudotyped HBV, and other cells. Human derived host
cells will assure that the anti-viral drug will enter the
cell efficiently and be converted by the cellular
15 enzymatic machinery into the metabolically relevant form
of the anti-viral inhibitor. Host cells are referred to
herein as a "packaging host cells," "resistance test
vector host cells," or "target host cells." A "packaging
host cell" refers to a host cell that provides the
20 trans-acting factors and viral packaging proteins required
by the replication defective viral vectors used herein,
such as the resistance test vectors, to produce resistance
test vector viral particles. The packaging proteins may
be provided for by the expression of viral genes contained
25 within the resistance test vector itself, a packaging
expression vector(s), or both. A packaging host cell is a
host cell which is transfected with one or more packaging
expression vectors and when transfected with a resistance
test vector is then referred to herein as a "resistance
30 test vector host cell" and is sometimes referred to as a
packaging host cell/resistance test vector host cell.
Preferred host cells for use as packaging host cells for
HIV include 293 human embryonic kidney cells (293, Graham,
F.L. et al., J. Gen Virol. 36: 59, 1977), BOSC23 (Pear et
35 al., *Proc. Natl. Acad. Sci.* **90**, 8392, 1993), tsa54 and
tsa201 cell lines (Heinzel et al., *J.Virol.* **62**,

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5 3738,1988), for HBV HepG2 (Galle and Theilmann, L.
Arzheim.-Forschy Drug Res. (1990) 40, 1380-1382). (Huh,
Ueda, K et al. Virology *1989) 169, 213-216). A "target
10 test vector viral particles produced by the resistance
test vector host cell in which expression or inhibition of
the indicator gene takes place. Preferred host cells for
use as target host cells include human T cell leukemia
cell lines including Jurkat (ATCC T1B-152), H9 (ATCC
HTB-176), CEM (ATCC CCL-119), HUT78 (ATCC T1B-161), and
15 derivatives thereof.

This invention is illustrated in the Experimental Details
section which follows. These sections are set forth to
aid in an understanding of the invention but are not
20 intended to, and should not be construed to, limit in any
way the invention as set forth in the claims which follow
thereafter.

Experimental Details

General Materials and Methods

25 Most of the techniques used to construct vectors, and
transfect and infect cells, are widely practiced in the
art, and most practitioners are familiar with the standard
resource materials that describe specific conditions and
30 procedures. However, for convenience, the following
paragraphs may serve as a guideline.

As used herein, "replication capacity" is defined herein
is a measure of how well the virus replicates. This may
35 also be referred to as viral fitness. In one embodiment,
replication capacity can be measured by evaluating the

5 ability of the virus to replicate in a single round of replication.

As used herein, "control resistance test vector" is defined as a resistance test vector comprising a standard
10 viral sequence (for example, HXB2, PNL4-3) and an indicator gene.

As used herein, "normalizing" is defined as standardizing the amount of the expression of indicator gene measured
15 relative to the number of viral particles giving rise to the expression of the indicator gene. For example, normalization is measured by dividing the amount of luciferase activity measured by the number of viral particles measured at the time of infection.

20 "Plasmids" and "vectors" are designated by a lower case p followed by letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed
25 from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

30 Construction of the vectors of the invention employs standard ligation and restriction techniques which are well understood in the art (see Ausubel et al., (1987) Current Protocols in Molecular Biology, Wiley - Interscience or Maniatis et al., (1992) in Molecular
35 Cloning: A laboratory Manual, Cold Spring Harbor Laboratory, N.Y.). Isolated plasmids, DNA sequences, or

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5 synthesized oligonucleotides are cleaved, tailored, and
religated in the form desired. The sequences of all DNA
constructs incorporating synthetic DNA were confirmed by
DNA sequence analysis (Sanger et al. (1977) Proc. Natl.
Acad. Sci. 74, 5463-5467).

10

"Digestion" of DNA refers to catalytic cleavage of the DNA
with a restriction enzyme that acts only at certain
sequences, restriction sites, in the DNA. The various
restriction enzymes used herein are commercially available
15 and their reaction conditions, cofactors and other
requirements are known to the ordinarily skilled artisan.
For analytical purposes, typically 1 µg of plasmid or DNA
fragment is used with about 2 units of enzyme in about 20
µl of buffer solution. Alternatively, an excess of
20 restriction enzyme is used to insure complete digestion of
the DNA substrate. Incubation times of about one hour to
two hours at about 37°C are workable, although variations
can be tolerated. After each incubation, protein is
removed by extraction with phenol/chloroform and the
25 nucleic acid recovered from aqueous fractions by
precipitation with ethanol. If desired, size separation
of the cleaved fragments may be performed by
polyacrylamide gel or agarose gel electrophoresis using
standard techniques. A general description of size
30 separations is found in Methods of Enzymology 65:499-560
(1980).

Restriction cleaved fragments may be blunt ended by
treating with the large fragment of E. coli DNA polymerase
35 I (Klenow) in the presence of the four deoxynucleotide
triphosphates (dNTPs) using incubation times of about 15

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5 to 25 minutes at 20°C in 50 mM Tris (pH 7.6) 50 mM NaCl, 6
mM MgCl₂, 6 mM DTT and 5-10 mM dNTPs. The Klenow fragment
fills in at 5' sticky ends but chews back protruding 3'
single strands, even though the four dNTPs are present.
If desired, selective repair can be performed by supplying
10 only one of the dNTPs, or with selected dNTPs, within the
limitations dictated by the nature of the sticky ends.
After treatment with Klenow, the mixture is extracted with
phenol/chloroform and ethanol precipitated. Treatment
under appropriate conditions with S1 nuclease or Bal-31
15 results in hydrolysis of any single-stranded portion.

Ligations are performed in 15-50 µl volumes under the
following standard conditions and temperatures: 20 mM
Tris-Cl pH 7.5, 10 mM MgCl₂, 10 mM DTT, 33 mg/ml BSA, 10
20 mM- 50 mM NaCl, and either 40 µM ATP, 0.01-0.02 (Weiss)
units T4 DNA ligase at 0°C (for "sticky end" ligation) or
1mM ATP, 0.3 - 0.6 (Weiss) units T4 DNA ligase at 14°C (for
"blunt end" ligation). Intermolecular "sticky end"
ligations are usually performed at 33-100 µg/ml total DNA
25 concentrations (5-100 mM total end concentration).
Intermolecular blunt end ligations (usually employing a
10-30 fold molar excess of linkers) are performed at 1µM
total ends concentration.

30 "Transient expression" refers to unamplified expression
within about one day to two weeks of transfection. The
optimal time for transient expression of a particular
desired heterologous gene may vary depending on several
factors including, for example, any transacting factors
35 which may be employed, translational control mechanisms
and the host cell. Transient expression occurs when the

5 particular plasmid that has been transfected functions,
i.e., is transcribed and translated. During this time the
plasmid DNA which has entered the cell is transferred to
the nucleus. The DNA is in a nonintegrated state, free
within the nucleus. Transcription of the plasmid taken up
10 by the cell occurs during this period. Following
transfection the plasmid DNA may become degraded or
diluted by cell division. Random integration within the
cell chromatin occurs.

15 In general, vectors containing promoters and control
sequences which are derived from species compatible with
the host cell are used with the particular host cell.
Promoters suitable for use with prokaryotic hosts
illustratively include the beta-lactamase and lactose
20 promoter systems, alkaline phosphatase, the tryptophan
(trp) promoter system and hybrid promoters such as tac
promoter. However, other functional bacterial promoters
are suitable. In addition to prokaryotes, eukaryotic
microbes such as yeast cultures may also be used.
25 *Saccharomyces cerevisiae*, or common baker's yeast is the
most commonly used eukaryotic microorganism, although a
number of other strains are commonly available. Promoters
controlling transcription from vectors in mammalian host
cells may be obtained from various sources, for example,
30 the genomes of viruses such as: polyoma, simian virus 40
(SV40), adenovirus, retroviruses, hepatitis B virus and
preferably cytomegalovirus, or from heterologous mammalian
promoters, e.g. β -actin promoter. The early and late
promoters of the SV 40 virus are conveniently obtained as
35 an SV40 restriction fragment that also contains the SV40
viral origin of replication. The immediate early promoter

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5 of the human cytomegalovirus is conveniently obtained as a
HindIII E restriction fragment. Of course, promoters from
the host cell or related species also are useful herein.

10 The vectors used herein may contain a selection gene, also
termed a selectable marker. A selection gene encodes a
protein, necessary for the survival or growth of a host
cell transformed with the vector. Examples of suitable
selectable markers for mammalian cells include the
15 dihydrofolate reductase gene (DHFR), the ornithine
decarboxylase gene, the multi-drug resistance gene (mdr),
the adenosine deaminase gene, and the glutamine synthase
gene. When such selectable markers are successfully
transferred into a mammalian host cell, the transformed
mammalian host cell can survive if placed under selective
20 pressure. There are two widely used distinct categories
of selective regimes. The first category is based on a
cell's metabolism and the use of a mutant cell line which
lacks the ability to grow independent of a supplemented
media. The second category is referred to as dominant
25 selection which refers to a selection scheme used in any
cell type and does not require the use of a mutant cell
line. These schemes typically use a drug to arrest growth
of a host cell. Those cells which have a novel gene would
express a protein conveying drug resistance and would
30 survive the selection. Examples of such dominant
selection use the drugs neomycin (Southern and Berg (1982)
J. Molec. Appl. Genet. 1, 327), mycophenolic acid
(Mulligan and Berg (1980) Science 209, 1422), or
hygromycin (Sugden et al. (1985) Mol. Cell. Biol. 5,
35 410-413). The three examples given above employ bacterial
genes under eukaryotic control to convey resistance to the

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5 appropriate drug neomycin (G418 or genticin), xgpt
(mycophenolic acid) or hygromycin, respectively.

10 "Transfection" means introducing DNA into a host cell so
that the DNA is expressed, whether functionally expressed
or otherwise; the DNA may also replicate either as an
extrachromosomal element or by chromosomal integration.
Unless otherwise provided, the method used herein for
transfection of the host cells is the calcium phosphate
co-precipitation method of Graham and van der Eb (1973)
15 Virology 52, 456-457. Alternative methods for
transfection are electroporation, the DEAE-dextran method,
lipofection and biolistics (Kriegler (1990) Gene Transfer
and Expression: A Laboratory Manual, Stockton Press).

20 Host cells may be transfected with the expression vectors
of the present invention and cultured in conventional
nutrient media modified as is appropriate for inducing
promoters, selecting transformants or amplifying genes.
Host cells are cultured in F12:DMEM (Gibco) 50:50 with
25 added glutamine. The culture conditions, such as
temperature, pH and the like, are those previously used
with the host cell selected for expression, and will be
apparent to the ordinarily skilled artisan.

30 The following examples merely illustrate the best mode now
known for practicing the invention, but should not be
construed to limit the invention. All publications and
patent applications cited in this specification are herein
incorporated by reference in their entirety as if each
35 individual publication or patent application were
specifically and individually indicated to be incorporated

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5 by reference.

EXAMPLE 1

Phenotypic Drug Susceptibility and Resistance Test Using Resistance Test Vectors

10 Phenotypic drug susceptibility and resistance tests are
carried out using the means and methods described in US
Patent Number 5,837,464 (International Publication Number
WO 97/27319) which is hereby incorporated by reference.

15 In these experiments patient-derived segment(s)
corresponding to the HIV -- protease and reverse
transcriptase coding regions were either patient-derived
segments amplified by the reverse transcription-polymerase
chain reaction method (RT-PCR) using viral RNA isolated
20 from viral particles present in the serum of HIV-infected
individuals or were mutants of wild type HIV-1 made by
site directed mutagenesis of a parental clone [^] of
resistance test vector DNA. Isolation of viral RNA was
performed using standard procedures (e.g. RNAagents Total
25 RNA Isolation System, Promega, Madison WI or RNazol,
Tel-Test, Friendswood, TX). The RT-PCR protocol was
divided into two steps. A retroviral reverse
transcriptase [e.g. Moloney MuLV reverse transcriptase
(Roche Molecular Systems, Inc., Branchburg, NJ), or avian
30 myeloblastosis virus (AMV) reverse transcriptase,
(Boehringer Mannheim, Indianapolis, IN)] was used to copy
viral RNA into cDNA. The cDNA was then amplified using a
thermostable DNA polymerase [e.g. Taq (Roche Molecular
Systems, Inc., Branchburg, NJ), Tth (Roche Molecular
35 Systems, Inc., Branchburg, NJ), PrimeZyme (isolated from
Thermus brockianus, Biometra, Gottingen, Germany)] or a

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5 combination of thermostable polymerases as described for
the performance of "long PCR" (Barnes, W.M., (1994) Proc.
Natl. Acad. Sci, USA 91, 2216-2220) [e.g. Expand High
Fidelity PCR System (Taq + Pwo), (Boehringer Mannheim.
Indianapolis, IN) OR GeneAmp XL PCR kit (Tth + Vent),
10 (Roche Molecular Systems, Inc., Branchburg, NJ)].

PCR6 (Table 5, #1) is used for reverse transcription of
viral RNA into cDNA. The primers, ApaI primer (PDSApa,
Table 5, #2) and AgeI primer (PDSAge, Table 5, #3) used to
15 amplify the "test" patient-derived segments contained
sequences resulting in ApaI and AgeI recognition sites
being introduced into both ends of the PCR product,
respectively.

Resistance test vectors incorporating the "test"
20 patient-derived segments were constructed as described in
US Patent Number 5,837,464 (International Publication
Number WO 97/27319) (see Fig. 1) using an amplified DNA
product of 1.5 kB prepared by RT-PCR using viral RNA as a
template and oligonucleotides PCR6 (#1), PDSApa (#2) and
25 PDSAge (#3) as primers, followed by digestion with ApaI
and AgeI or the isoschizomer PnaI. To ensure that the
plasmid DNA corresponding to the resultant resistance test
vector comprises a representative sample of the HIV viral
quasi-species present in the serum of a given patient,
30 many (>100) independent E. coli transformants obtained in
the construction of a given resistance test vector were
pooled and used for the preparation of plasmid DNA.

A packaging expression vector encoding an amphotrophic
35 MuLV 4070A env gene product enables production in a
resistance test vector host cell of resistance test vector

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5 viral particles which can efficiently infect human target
cells. Resistance test vectors encoding all HIV genes
with the exception of env were used to transfect a
packaging host cell (once transfected the host cell is
referred to as a resistance test vector host cell). The
10 packaging expression vector which encodes the amphotrophic
MuLV 4070A env gene product is used with the resistance
test vector to enable production in the resistance test
vector host cell of infectious pseudotyped resistance test
vector viral particles.

15 Resistance tests performed with resistance test vectors
were carried out using packaging host and target host
cells consisting of the human embryonic kidney cell line
293 (Cell Culture Facility, UC San Francisco, SF, CA) or
20 the Jurkat leukemic T-cell line (Arthur Weiss, UC San
Francisco, SF, CA).

Resistance tests were carried out with resistance test
vectors using two host cell types. Resistance test vector
25 viral particles were produced by a first host cell (the
resistance test vector host cell) that was prepared by
transfecting a packaging host cell with the resistance
test vector and the packaging expression vector. The
resistance test vector viral particles were then used to
30 infect a second host cell (the target host cell) in which
the expression of the indicator gene is measured (see Fig.
2).

The resistance test vectors containing a functional
35 luciferase gene cassette were constructed and host cells
were transfected with the resistance test vector DNA. The

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5 resistant test vectors contained patient-derived reverse
transcriptase and protease DNA sequences that encode
proteins which were either susceptible or resistant to the
antiretroviral agents, such as nucleoside reverse
transcriptase inhibitors, non-nucleoside reverse
10 transcriptase inhibitors and protease inhibitors. The
resistance test vector viral particles produced by
transfecting the resistance test vector DNA into host
cells, either in the presence or absence of protease
inhibitors, were used to infect target host cells grown
15 either in the absence of NRTI or NNRTI or in the presence
of increasing concentrations of the drug. Luciferase
activity in infected target host cells in the presence of
drug was compared to the luciferase activity in infected
target host cells in the absence of drug. Drug resistance
20 was measured as the concentration of drug required to
inhibit by 50% the luciferase activity detected in the
absence of drug (inhibitory concentration 50%, IC₅₀).
The IC₅₀ values were determined by plotting percent drug
inhibition vs. log₁₀ drug concentration.

25 Host cells were seeded in 10-cm-diameter dishes and were
transfected one day after plating with resistance test
vector plasmid DNA and the envelope expression vector.
Transfections were performed using a calcium-phosphate
30 co-precipitation procedure. The cell culture media
containing the DNA precipitate was replaced with fresh
medium, from one to 24 hours, after transfection. Cell
culture media containing resistance test vector viral
particles was harvested one to four days after
35 transfection and was passed through a 0.45-mm filter
before being stored at -80°C. HIV capsid protein (p24)

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5 levels in the harvested cell culture media were determined
by an EIA method as described by the manufacturer (SIAC;
Frederick, MD). Before infection, target cells (293 and
293/T) were plated in cell culture media. Control
infections were performed using cell culture media from
10 mock transfections (no DNA) or transfections containing
the resistance test vector plasmid DNA without the
envelope expression plasmid. One to three or more days
after infection the media was removed and cell lysis
buffer (Promega) was added to each well. Cell lysates
15 were assayed for luciferase activity. The inhibitory
effect of the drug was determined using the following
equation:

$$\% \text{ luciferase inhibition} = \frac{[1 - (\text{RLU}_{\text{luc}} [\text{drug}] / \text{RLU}_{\text{luc}})] \times 100}{100}$$

where $\text{RLU}_{\text{luc}} [\text{drug}]$ is the relative light unit of
luciferase activity in infected cells in the presence of
drug and RLU_{luc} is the Relative Light Unit of luciferase
25 activity in infected cells in the absence of drug. IC50
values were obtained from the sigmoidal curves that were
generated from the data by plotting the percent inhibition
of luciferase activity vs. the \log_{10} drug concentration.
Examples of drug inhibition curves are shown in (Fig. 3).

30

EXAMPLE 2

**An in vitro Assay Using Resistance Test Vectors And Site
Directed Mutants To Correlate Phenotypes And Genotypes
Associated With HIV Drug Susceptibility And Resistance**
35 Phenotypic susceptibility analysis of patient HIV samples
Resistance test vectors are constructed as described in

5 example 1. Resistance test vectors, or clones derived from
the resistance test vector pools, are tested in a
phenotypic assay to determine accurately and
quantitatively the level of susceptibility to a panel of
10 anti-retroviral drugs. This panel of anti-retroviral
drugs may comprise members of the classes known as
nucleoside-analog reverse transcriptase inhibitors
(NRTIs), non-nucleoside reverse transcriptase inhibitors
(NNRTIs), and protease inhibitors (PRIs). The panel of
15 drugs can be expanded as new drugs or new drug targets
become available. An IC50 is determined for each
resistance test vector pool for each drug tested. The
pattern of susceptibility to all of the drugs tested is
examined and compared to known patterns of susceptibility.

20 A patient sample can be further examined for genotypic
changes correlated with the pattern of susceptibility
observed.

Genotypic analysis of patient HIV samples

25 Resistance test vector DNAs, either pools or clones, are
analyzed by any of the genotyping methods described in
Example 1. In one embodiment of the invention, patient
HIV sample sequences are determined using viral RNA
purification, RT/PCR and ABI chain terminator automated
30 sequencing. The sequence that is determined is compared
to control sequences present in the database or is
compared to a sample from the patient prior to initiation
of therapy, if available. The genotype is examined for
sequences that are different from the control or
pre-treatment sequence and correlated to the observed
35 phenotype.

5 **Phenotypic susceptibility analysis of site directed mutants**

Genotypic changes that are observed to correlate with changes in phenotypic patterns of drug susceptibility are evaluated by construction of resistance test vectors containing the specific mutation on a defined, wild-type (drug susceptible) genetic background. Mutations may be incorporated alone and/or in combination with other mutations that are thought to modulate the susceptibility of HIV to a certain drug or class of drugs. Mutations are introduced into the resistance test vector through any of the widely known methods for site-directed mutagenesis. In one embodiment of this invention the mega-primer PCR method for site-directed mutagenesis is used. A resistance test vector containing the specific mutation or group of mutations are then tested using the phenotypic susceptibility assay described above and the susceptibility profile is compared to that of a genetically defined wild-type (drug susceptible) resistance test vector which lacks the specific mutations. Observed changes in the pattern of phenotypic susceptibility to the antiretroviral drugs tested are attributed to the specific mutations introduced into the resistance test vector.

30 **EXAMPLE 3**

Using Resistance Test Vectors To Correlate Genotypes And Phenotypes Associated With Changes in PRI Drug Susceptibility in HIV.

Phenotypic analysis of Patient 0732

35 A resistance test vector was constructed as described in example 1 from a patient sample designated as 0732. This

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5 patient had been previously treated with nelfinavir. Isolation of viral RNA and RT/PCR was used to generate a patient derived segment that comprised viral sequences coding for all of PR and aa 1 - 313 of RT. The patient derived segment was inserted into an indicator gene viral
10 vector to generate a resistance test vector designated RTV-0732. RTV-0732 was tested using a phenotypic susceptibility assay to determine accurately and quantitatively the level of susceptibility to a panel of anti-retroviral drugs. This panel of anti-retroviral
15 drugs comprised members of the classes known as NRTIs (AZT, 3TC, d4T, ddI, ddC, and abacavir), NNRTIs (delavirdine, nevirapine and efavirenz), and PRIs (indinavir, nelfinavir, ritonavir, saquinavir and amprenavir). An IC50 was determined for each drug tested. Susceptibility of the patient virus to each drug was
20 examined and compared to known patterns of susceptibility. A pattern of susceptibility to the PRIs was observed for patient sample RTV-0732 in which there was a decrease in both nelfinavir and indinavir susceptibility (increased resistance) and an increase in amprenavir susceptibility
25 (see Fig. 4 and Table 1). Patient sample 0732 was examined further for genotypic changes associated with the pattern of susceptibility.

30 **Determination of genotype of patient 0732**

RTV-0732 DNA was analyzed by ABI chain terminator automated sequencing. The nucleotide sequence was compared to the consensus sequence of a wild type clade B HIV-1 (HIV Sequence Database Los Alamos, NM). The
35 nucleotide sequence was examined for sequences that are different from the control sequence. PR mutations were

5 noted at positions K14R, I15V, K20T, E35D, M36I, R41K,
I62V, L63Q and N88S. K14R, I15V, E35D, R41K and I62V are
naturally occurring polymorphisms in HIV-1 PR and are not
associated with reduced susceptibility to any drug. M36I
has previously been described to be associated with
10 resistance to ritonavir and nelfinavir (Shihazi, 1998).
N88S has previously been described to be associated with
resistance to nelfinavir (Patick AAC, 42: 2637 (1998) and
an investigational PRI, SC55389A (Smidt, 1997).

15 **Phenotypic analysis of Patient 627**

A resistance test vector was constructed as described in
example 1 from a patient sample designated as 627. This
patient had been treated with indinavir. Isolation of
viral RNA and RT/PCR was used to generate a patient
20 derived segment that comprised viral sequences coding for
all of PR and aa 1 - 313 of RT. The patient derived
segment was inserted into an indicator gene viral vector
to generate a resistance test vector designated RTV-627.
RTV-627 was tested using a phenotypic susceptibility assay
25 to determine accurately and quantitatively the level of
susceptibility to a panel of anti-retroviral drugs. This
panel of anti-retroviral drugs comprised members of the
classes known as NRTIs (AZT, 3TC, d4T, ddI, ddC, and
abacavir), NNRTIs (delavirdine, nevirapine and efavirenz),
30 and PRIs (indinavir, nelfinavir, ritonavir, saquinavir and
amprenavir). An IC50 was determined for each drug tested.
Susceptibility of the patient virus to each drug was
examined and compared to known patterns of susceptibility.
A pattern of susceptibility to the PRIs was observed for
35 patient sample RTV-627 in which there was a decrease in
indinavir and nelfinavir susceptibility (increased

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5 resistance) and an increase in amprenavir and saquinavir susceptibility. Patient sample 627 was examined further for genotypic changes associated with the pattern of susceptibility.

10 **Determination of genotype of patient 627**

RTV-627 DNA was analyzed by ABI chain terminator automated sequencing. The nucleotide sequence was compared to the consensus sequence of a wild type clade B HIV-1 (HIV Sequence Database Los Alamos, NM). The nucleotide
15 sequence was examined for sequences that are different from the control sequence. PR mutations were noted at positions 13I/V, E35D, M46L, L63P, I64V, I73V and N88S. I13V, E35D and I64V are naturally occurring polymorphisms in HIV-1 PR and are not associated with reduced
20 susceptibility to any drug. M46L has previously been described to be associated with resistance to indinavir and amprenavir. L63P has previously been described to be associated with resistance to indinavir and nelfinavir. N88S has previously been described to be associated with
25 resistance to nelfinavir (Patick, 1998) and an investigational PRI, SC55389A (Smidt, 1997).

Phenotypic analysis of Patient 1208

A resistance test vector was constructed as described in
30 example 1 from a patient sample designated as 1208. This patient had been previously treated with nelfinavir. Isolation of viral RNA and RT/PCR was used to generate a patient derived segment that comprised viral sequences coding for all of PR and aa 1 - 313 of RT. The patient
35 derived segment was inserted into an indicator gene viral vector to generate a resistance test vector designated

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5 RTV-1208. RTV-1208 was tested using a phenotypic
susceptibility assay to determine accurately and
quantitatively the level of susceptibility to a panel of
anti-retroviral drugs. This panel of anti-retroviral drugs
10 comprised members of the classes known as NRTIs (AZT, 3TC,
d4T, ddI, ddC, and abacavir), NNRTIs (delavirdine,
nevirapine and efavirenz), and PRIs (indinavir,
nelfinavir, ritonavir, saquinavir and amprenavir). An IC50
was determined for each drug tested. Susceptibility of
the patient virus to each drug was examined and compared
15 to known patterns of susceptibility. A pattern of
susceptibility to the PRIs was observed for patient sample
RTV-1208 in which there was a decrease in indinavir and
nelfinavir susceptibility (increased resistance) and an
increase in amprenavir susceptibility. Patient sample
20 1208 was examined further for genotypic changes associated
with the pattern of susceptibility.

Determination of genotype of patient 1208

RTV-1208 DNA was analyzed by ABI chain terminator
25 automated sequencing. The nucleotide sequence was
compared to the consensus sequence of a wild type clade B
HIV-1 (HIV Sequence Database Los Alamos, NM). The
nucleotide sequence was examined for sequences that are
different from the control sequence. PR mutations were
30 noted at positions I62V, L63P, V77I, and N88S. I62V is a
naturally occurring polymorphism in HIV-1 PR and is not
associated with reduced susceptibility to any drug. L63P
has previously been described to be associated with
resistance to indinavir and nelfinavir. V77I has
35 previously been described to be associated with resistance
to nelfinavir. N88S has previously been described to be

5 associated with resistance to nelfinavir (Patick, 1998)
and an investigational PRI, SC55389A (Smidt, 1997).

10 **Phenotypic analysis of Patient 360**

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15 A resistance test vector was constructed as described in
example 1 from a patient sample designated as 360. This
patient had been previously treated with indinavir.
Isolation of viral RNA and RT/PCR was used to generate a
patient derived segment that comprised viral sequences
coding for all of PR and aa 1 - 313 of RT. The patient
derived segment was inserted into an indicator gene viral
vector to generate a resistance test vector designated
RTV-360. RTV-360 was tested using a phenotypic
20 susceptibility assay to determine accurately and
quantitatively the level of susceptibility to a panel of
anti-retroviral drugs. This panel of anti-retroviral drugs
comprised members of the classes known as NRTIs (AZT, 3TC,
d4T, ddI, ddC, and abacavir), NNRTIs (delavirdine,
25 nevirapine and efavirenz), and PRIs (indinavir,
nelfinavir, ritonavir, saquinavir and amprenavir). An IC50
was determined for each drug tested. Susceptibility of
the patient virus to each drug was examined and compared
to known patterns of susceptibility. A pattern of
30 susceptibility to the PRIs was observed for patient sample
RTV-360 in which there was a decrease in indinavir and
nelfinavir susceptibility (increased resistance) and an
increase in amprenavir susceptibility. Patient sample 360
was examined further for genotypic changes associated with
35 the pattern of susceptibility.

5 **Determination of genotype of patient 360**

RTV-360 DNA was analyzed by ABI chain terminator automated sequencing. The nucleotide sequence was compared to the consensus sequence of a wild type clade B HIV-1 (HIV Sequence Database Los Alamos, NM). The nucleotide sequence was examined for sequences that are different from the control sequence. PR mutations were noted at positions I13V, K20M, M36V, N37A, M46I, I62V, L63P, N88S, and I93L. I13V, N37A and I62V are naturally occurring polymorphisms in HIV-1 PR and are not associated with reduced susceptibility to any drug. K20M has previously been described to be associated with resistance to indinavir. M46I has previously been described to be associated with resistance to indinavir, ritonavir, nelfinavir and amprenavir. L63P has previously been described to be associated with resistance to indinavir and nelfinavir. N88S has previously been described to be associated with resistance to nelfinavir (Patick, 1998) and an investigational PRI, SC55389A (Smidt, 1997).

25 **Phenotypic analysis of Patient 0910**

A resistance test vector was constructed as described in example 1 from a patient sample designated as 0910. This patient had been previously treated with nelfinavir. Isolation of viral RNA and RT/PCR was used to generate a patient derived segment that comprised viral sequences coding for all of PR and aa 1 - 313 of RT. The patient derived segment was inserted into an indicator gene viral vector to generate a resistance test vector designated RTV-0910. RTV-0910 was tested using a phenotypic susceptibility assay to determine accurately and quantitatively the level of susceptibility to a panel of

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5 anti-retroviral drugs. This panel of anti-retroviral drugs
comprised members of the classes known as NRTIs (AZT, 3TC,
d4T, ddI, ddC, and abacavir), NNRTIs (delavirdine,
nevirapine and efavirenz), and PRIs (indinavir,
nelfinavir, ritonavir, saquinavir and amprenavir). An IC50
10 was determined for each drug tested. Susceptibility of
the patient virus to each drug was examined and compared
to known patterns of susceptibility. A pattern of
susceptibility to the PRIs was observed for patient sample
RTV-0910 in which there was a decrease in indinavir and
15 nelfinavir susceptibility (increased resistance) and an
increase in amprenavir susceptibility. Patient sample
0910 was examined further for genotypic changes associated
with the pattern of susceptibility.

20 **Determination of genotype of patient 0910**

RTV-0910 DNA was analyzed by ABI chain terminator
A automated sequencing. The nucleotide sequence was
compared to the consensus sequence of a wild type clade B
HIV-1 (HIV Sequence Database Los Alamos, NM). The
25 nucleotide sequence was examined for sequences that are
different from the control sequence. PR mutations were
noted at positions M46I, L63P, V77I, N88S and I93I/L.
I13V, K14R, N37D and I193L are naturally occurring
polymorphism in HIV-1 PR and is not associated with
30 reduced susceptibility to any drug. V77I has previously
been described to be associated with resistance to
nelfinavir. M46I has previously been described to be
associated with resistance to indinavir, ritonavir,
nelfinavir and amprenavir. L63P has previously been
35 described to be associated with resistance to indinavir
and nelfinavir. N88S has previously been described to be

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5 associated with resistance to nelfinavir (Patick, 1998)
and an investigational PRI, SC55389A (Smidt, 1997).

Phenotypic analysis of Patient 3542

10 A resistance test vector was constructed as described in
example 1 from a patient sample designated as 3542. This
patient had been treated with indinavir. Isolation of
viral RNA and RT/PCR was used to generate a patient
derived segment that comprised viral sequences coding for
all of PR and aa 1 - 313 of RT. The patient derived
15 segment was inserted into an indicator gene viral vector
to generate a resistance test vector designated RTV-3542.
RTV-3542 was tested using a phenotypic susceptibility
assay to determine accurately and quantitatively the level
of susceptibility to a panel of anti-retroviral drugs.
20 This panel of anti-retroviral drugs comprised members of
the classes known as NRTIs (AZT, 3TC, d4T, ddI, ddC, and
abacavir), NNRTIs (delavirdine, nevirapine and efavirenz),
and PRIs (indinavir, nelfinavir, ritonavir, saquinavir and
amprenavir). An IC50 was determined for each drug tested.
25 Susceptibility of the patient virus to each drug was
examined and compared to known patterns of susceptibility.
A pattern of susceptibility to the PRIs was observed for
patient sample RTV-3542 in which there was a decrease in
indinavir, nelfinavir and ritonavir susceptibility
30 (increased resistance) and an increase in amprenavir
susceptibility. Patient sample 3542 was examined further
for genotypic changes associated with the pattern of
susceptibility.

35 Determination of genotype of patient 3542
RTV-3542 DNA was analyzed by ABI chain terminator

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5 automated sequencing. The nucleotide sequence was
compared to the consensus sequence of a wild type clade B
HIV-1 (HIV Sequence Database Los Alamos, NM). The
nucleotide sequence was examined for sequences that are
different from the control sequence. PR mutations were
10 noted at positions I13V, K14R, N37D, M46I, L63P, N88S and
I93L. K14R and N37A/D are naturally occurring
polymorphisms in HIV-1 PR and are not associated with
reduced susceptibility to any drug. M46I has previously
been described to be associated with resistance to
15 indinavir, ritonavir, nelfinavir and amprenavir. L63P has
previously been described to be associated with resistance
to indinavir and nelfinavir. N88S has previously been
described to be associated with resistance to nelfinavir
(Patick, 1998) and an investigational PRI, SC55389A
20 (Smidt, 1997).

Phenotypic analysis of Patient 3654 ^

A resistance test vector was constructed as described in
example 1 from a patient sample designated as 3654. This
25 patient had been previously treated with ritonavir.
Isolation of viral RNA and RT/PCR was used to generate a
patient derived segment that comprised viral sequences
coding for all of PR and aa 1 - 313 of RT. The patient
derived segment was inserted into an indicator gene viral
30 vector to generate a resistance test vector designated
RTV-3654. RTV-3654 was tested using a phenotypic
susceptibility assay to determine accurately and
quantitatively the level of susceptibility to a panel of
anti-retroviral drugs. This panel of anti-retroviral drugs
35 comprised members of the classes known as NRTIs (AZT, 3TC,
d4T, ddI, ddC, and abacavir), NNRTIs (delavirdine,

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5 nevirapine and efavirenz), and PRIs (indinavir, nelfinavir, ritonavir, saquinavir and amprenavir). An IC50 was determined for each drug tested. Susceptibility of the patient virus to each drug was examined and compared to known patterns of susceptibility. A pattern of
10 susceptibility to the PRIs was observed for patient sample RTV-3654 in which there was a decrease in indinavir and nelfinavir susceptibility (increased resistance) and an increase in amprenavir susceptibility. Patient sample 3654 was examined further for genotypic changes associated
15 with the pattern of susceptibility.

Determination of genotype of patient 3654

RTV-3654 DNA was analyzed by ABI chain terminator automated sequencing. The nucleotide sequence was
20 compared to the consensus sequence of a wild type clade B HIV-1 (HIV Sequence Database Los Alamos, NM). The nucleotide sequence was examined for sequences that are different from the control sequence. PR mutations were noted at positions I13V, R41K, M46I, L63P, V77I, N88S and
25 I93L. I13V, R41K and I93L are naturally occurring polymorphism in HIV-1 PR and is not associated with reduced susceptibility to any drug. M46I has previously been described to be associated with resistance to indinavir, ritonavir, nelfinavir and amprenavir. L63P has
30 previously been described to be associated with resistance to indinavir and nelfinavir. V77I has previously been described to be associated with resistance to nelfinavir. N88S has previously been described to be associated with resistance to an investigational PRI, SC55389A (Smidt,
35 1997).

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EXAMPLE 4

Using Site Directed Mutants To Correlate Genotypes And Phenotypes Associated With Changes in PRI Drug Susceptibility in HIV.

Site directed mutagenesis

10 Resistance test vectors were constructed containing the
N88S mutation alone and in combination with other
substitutions in PR (L63P, V77I and M46L) known to
modulate the HIV susceptibility to PRIs. Mutations were
introduced into the resistance test vector using the
15 mega-primer PCR method for site-directed mutagenesis.
(Sakar G and Sommar SS (1994) Biotechniques 8(4),
404-407). First, a resistance test vector was constructed
that harbors a unique RsrII restriction site 590 bp
downstream of the ApaI restriction site. The 590 bp ApaI
20 - RsrII fragment thus contains the entire protease region.
This site was introduced by site-specific
oligonucleotide-directed mutagenesis using primer #4. All
subsequent mutants were constructed by fragment-exchange
of the wild-type ApaI - RsrII fragment in the parent
25 vector with the equivalent fragment carrying the
respective mutations.

A resistance test vector containing the N88S mutation
(N88S-RTV) was tested using the phenotypic susceptibility
30 assay described above and the results were compared to
that of a genetically defined resistance test vector that
was wild type at position 88. The pattern of phenotypic
susceptibility to the PRIs in the N88S-RTV was altered as
compared to wild type. In the context of an otherwise
35 wild type background (i.e. N88S mutation alone) the
N88S-RTV was more susceptible to both amprenavir and.

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5 ritonavir and slightly less susceptible to nelfinavir
compared to the wild type control RTV (see Table 2).

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10 A resistance test vector containing the N88S mutation
along with the L63P mutation (L63P-N88S-RTV) was tested
using the phenotypic susceptibility assay described above
and the results were compared to that of a genetically
defined resistance test vector that was wild type at
positions 63 and 88. The L63P-N88S-RTV showed decreased
susceptibility to both indinavir and nelfinavir and an
15 increase in the susceptibility to amprenavir compared the
wild-type control RTV (see Table 2). Thus it appears that
the introduction of a second mutation, L63P, in addition
to N88S, results in a reduction in susceptibility to
nelfinavir and indinavir while the increased
20 susceptibility to amprenavir is maintained.

25 A [^]resistance test vector containing the N88S mutation
along with the L63P mutation and the V77I mutation
(L63P-V77I-N88S-RTV) was tested using the phenotypic
susceptibility assay described above and the results were
compared to that of a genetically defined resistance test
vector that was wild type at positions 63 and 77 and 88.
The RTV containing mutations at these positions,
L63P-V77I-N88S-RTV, showed a decrease in susceptibility to
30 both indinavir and nelfinavir and an increase in the
susceptibility to amprenavir compared to the wild-type
control RTV (see Fig. 5 and Table 2). Thus it appears
that the introduction of a third mutation, V77I, in
addition to L63P and N88S, results in a reduction in
35 susceptibility to nelfinavir and indinavir while the
increased susceptibility to amprenavir is maintained.

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The N88S mutation was also introduced into an RTV containing additional mutations at positions L63P and M46L (M46L + L63P + N88S). The RTV containing mutations at these positions, M46L-L63P-N88S-RTV showed a decrease in susceptibility to nelfinavir and a slight decrease in susceptibility to indinavir and an increase in the susceptibility to amprenavir compared to the wild-type control RTV (see Fig. 5 and Table 2). Thus it appears that the introduction of a third mutation, M46L, in addition to L63P and N88S, results in a reduction in susceptibility to nelfinavir and indinavir while the increased susceptibility to amprenavir is maintained.

A resistance test vector containing the N88S mutation along with the M46L mutation, the L63P mutation, and the V77I mutation (M46L-L63P-V77I-N88S-RTV) was tested using the phenotypic susceptibility assay described above and the results were compared to that of a genetically defined resistance test vector that was wild type at positions 46, 63, 77 and 88. The RTV containing mutations at these four positions, M46L-L63P-V77I-N88S-RTV showed a decrease in susceptibility to nelfinavir and indinavir and an increase in the susceptibility to amprenavir compared to the wild-type control RTV (see Fig. 5 and Table 2). Thus it appears that the introduction of a fourth mutation, V77I, in addition to L63P, M46L and N88S results in a reduction in susceptibility to nelfinavir and indinavir while the increased susceptibility to amprenavir is maintained.

A resistance test vector containing the L63P mutation (L63P-RTV) was tested using the phenotypic susceptibility assay described above and the results were compared to

5 that of a genetically defined resistance test vector that was wild type at position 63. The pattern of phenotypic susceptibility to the PRIs in the L63P-RTV was similar to wild type with no significant changes in susceptibility to the PRIs observed.

10

The L63P mutation was also introduced into an RTV containing an additional mutation at position V77I. The L63P-V77I-RTV showed a slight decrease in susceptibility to nelfinavir compared to the wild-type control RTV (see Fig. 5 and Table 2).

15

EXAMPLE 5

Predicting Response to Protease Inhibitors by Characterization of Amino Acid 88 of HIV-1 Protease.

20

In one embodiment of this invention, changes in the amino acid at position 88 of the protease protein of HIV₁ is evaluated using the following method comprising: (i) collecting a biological sample from an HIV-1 infected subject; (ii) evaluating whether the biological sample contains nucleic acid encoding HIV-1 protease having an asparagine to serine mutation at codon 88 (N88S); and (iii) determining susceptibility to protease inhibitors (PRI).

25

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35

The biological sample comprises whole blood, blood components including peripheral mononuclear cells (PBMC), serum, plasma (prepared using various anticoagulants such as EDTA, acid citrate-dextrose, heparin), tissue biopsies, cerebral spinal fluid (CSF), or other cell, tissue or body fluids. In another embodiment, the HIV-1 nucleic acid

5 (genomic RNA) or reverse transcriptase protein can be
isolated directly from the biological sample or after
purification of virus particles from the biological
sample. Evaluating whether the amino acid at position 88
of the HIV-1 protease is mutated to serine, can be
10 performed using various methods, such as direct
characterization of the viral nucleic acid encoding
protease or direct characterization of the protease
protein itself. Defining the amino acid at position 88 of
protease can be performed by direct characterization of
15 the protease protein by conventional or novel amino acid
sequencing methodologies, epitope recognition by
antibodies or other specific binding proteins or
compounds. Alternatively, the amino acid at position 88
of the HIV-1 protease protein can be defined by
20 characterizing amplified copies of HIV-1 nucleic acid
encoding the protease protein. Amplification of the HIV-1
nucleic acid can be performed using a variety of
methodologies including reverse transcription-polymerase
chain reaction (RT-PCR), NASBA, SDA, RCR, or 3SR. The
25 nucleic acid sequence encoding HIV protease at codon 88
can be determined by direct nucleic acid sequencing using
various primer extension-chain termination (Sanger, ABI/PE
and Visible Genetics) or chain cleavage (Maxam and
Gilbert) methodologies or more recently developed
30 sequencing methods such as matrix assisted laser
desorption-ionization time of flight (MALDI-TOF) or mass
spectrometry (Sequenom, Gene Trace Systems).
Alternatively, the nucleic acid sequence encoding amino
acid position 88 can be evaluated using a variety of probe
35 hybridization methodologies, such as genechip
hybridization sequencing (Affymetrix), line probe assay

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5 (LiPA; Murex), and differential hybridization (Chiron).

10 In a preferred embodiment of this invention, evaluation of
protease inhibitor susceptibility and of whether amino
acid position 88 of HIV-1 protease was wild type or serine
was carried out using a phenotypic susceptibility assay or
genotypic assay, respectively, using resistance test
vector DNA prepared from the biological sample. In one
embodiment, the plasma sample was collected, viral RNA was
purified and an RT-PCR methodology was used to amplify a
15 patient derived segment encoding the HIV-1 protease and
reverse transcriptase regions. The amplified patient
derived segments were then incorporated, via DNA ligation
and bacterial transformation, into an indicator gene viral
vector thereby generating a resistance test vector.
20 Resistance test vector DNA was isolated from the bacterial
culture and the phenotypic susceptibility assay was
carried out as described in Example 1. The results of the
phenotypic susceptibility assay with a patient sample
having an N88S mutation in PR is shown in Figure 4. The
25 nucleic acid (DNA) sequence of the patient derived HIV-1
protease and reverse transcriptase regions from patient
sample 0732 was determined using a fluorescence detection
chain termination cycle sequencing methodology (ABI/PE).
The method was used to determine a consensus nucleic acid
30 sequence representing the combination of sequences of the
mixture of HIV-1 variants existing in the subject sample
(representing the quasispecies), and to determine the
nucleic acid sequences of individual variants.

35 **Phenotypic and genotypic correlation of mutations at amino
acid 88 of HIV-1 Protease.**

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5 Phenotypic susceptibility profiles of patient samples and
site directed mutants showed that amprenavir
susceptibility correlated with the presence of the N88S
mutation in HIV-1 protease. Phenotypic susceptibility
10 profiles of patient samples and site directed mutants
showed that a significant increase in amprenavir
susceptibility (decreased resistance) correlated with a
mutation in the nucleic acid sequence encoding the amino
acid serine (S) at position 88 of HIV-1 protease.

15 Phenotypic susceptibility profiles of patient samples and
site directed mutants showed reduction in amprenavir
susceptibility (decreased resistance) and a decrease in
susceptibility to nelfinavir and indinavir with the amino
acid serine at position 88 when the PR mutations at
20 positions 63, 77 or 46 were also present (L63P, V77I, or
M46L).

EXAMPLE 6

25 **Using Resistance test vectors and site directed mutants to
correlate genotypes associated with alterations in PRI
susceptibility with viral fitness.**

Luciferase activity measured in the absence of drug for
30 the seven resistance test vectors constructed from the
patient viruses containing the N88S PR mutation ranged
from 0.7 to 16% of control (Table 3). Although these
viruses also contain multiple mutations in reverse
transcriptase, which could also contribute to a reduction
35 in viral fitness, the data suggest that viruses containing
the N88S mutation are less fit than wild type. To confirm

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5 this observation, the luciferase expression level for the
site-directed mutant resistance test vectors was also
examined.

10 Viruses containing N88S as the only substitution produced
only 1.0% of the luciferase activity in the absence of
drug (Table 4). This reduction was substantially
alleviated by the addition of the L63P substitution
(20.7%) or by addition of the combinations of L63P/V77I
(29.3%) or M46L/L63P (28.0%). The L63P or L63P/V77I
15 mutants had equivalent or increased relative luciferase
activity compared to wild type (163.9 and 75.6%,
respectively).

20 When the K20T substitution was added to the N88S
background, either alone or in combination with L63P, only
background levels of luciferase activity was detected.
Sequence analysis confirmed the absence of additional
mutations, which might render the vector inactive. Thus
the combination of the K20T and N88S substitutions
25 correlates with a severe defect in fitness.

EXAMPLE 7

Predicting Response to Protease Inhibitors by Characterization of Amino Acid 82 of HIV-1 30 Protease.

35 In one embodiment of this invention, changes in the amino
acid at position 82 of the protease protein of HIV-1 are
evaluated using the following method comprising: (i)
collecting a biological sample from an HIV-1 infected
subject; (ii) evaluating whether the biological sample

5 contains nucleic acid encoding HIV-1 protease having a valine to alanine (V82A), phenylalanine (V82F), serine (V82S), or threonine (V82T) substitution at codon 82; and (iii) determining susceptibility to protease inhibitors (PRI).

10

The biological sample comprises whole blood, blood components including peripheral mononuclear cells (PBMC), serum, plasma (prepared using various anticoagulants such as EDTA, acid citrate-dextrose, heparin), tissue biopsies, 15 cerebral spinal fluid (CSF), or other cell, tissue or body fluids. In another embodiment, the HIV-1 nucleic acid (genomic RNA) or reverse transcriptase protein can be isolated directly from the biological sample or after purification of virus particles from the biological sample. Evaluating whether the amino acid at position 82 20 of the HIV-1 protease is mutated to alanine, phenylalanine, serine, or threonine, can be performed using various methods, such as direct characterization of the viral nucleic acid encoding protease or direct characterization of the protease protein itself. Defining 25 the amino acid at position 82 of protease can be performed by direct characterization of the protease protein by conventional or novel amino acid sequencing methodologies, epitope recognition by antibodies or other specific binding proteins or compounds. Alternatively, the amino 30 acid at position 82 of the HIV-1 protease protein can be defined by characterizing amplified copies of HIV-1 nucleic acid encoding the protease protein. Amplification of the HIV-1 nucleic acid can be performed using a variety of 35 methodologies including reverse transcription-polymerase chain reaction (RT-PCR), NASBA,

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5 SDA, RCR, or 3SR. The nucleic acid sequence encoding HIV
protease at codon 82 can be determined by direct nucleic
acid sequencing using various primer extension-chain
termination (Sanger, ABI/PE and Visible Genetics) or chain
10 cleavage (Maxam and Gilbert) methodologies or more
recently developed sequencing methods such as matrix
assisted laser desorption-ionization time of flight
(MALDI-TOF) or mass spectrometry (Sequenom, Gene Trace
Systems). Alternatively, the nucleic acid sequence
15 encoding amino acid position 82 can be evaluated using a
variety of probe hybridization methodologies, such as
genechip hybridization sequencing (Affymetrix), line probe
assay (LiPA; Murex), and differential hybridization
(Chiron).

20 In a preferred embodiment of this invention, evaluation of
protease inhibitor susceptibility and of whether amino
acid position 82 of HIV-1 protease was wild type or
alanine, phenylalanine, serine, or threonine, was carried
out using a phenotypic susceptibility assay or genotypic
25 assay, respectively, using resistance test vector DNA
prepared from the biological sample. In one embodiment,
the plasma sample was collected, viral RNA was purified
and an RT-PCR methodology was used to amplify a patient
derived segment encoding the HIV-1 protease and reverse
30 transcriptase regions. The amplified patient derived
segments were then incorporated, via DNA ligation and
bacterial transformation, into an indicator gene viral
vector thereby generating a resistance test vector.
Resistance test vector DNA was isolated from the bacterial
35 culture and the phenotypic susceptibility assay was
carried out and analyzed as described in Example 1.

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The nucleic acid (DNA) sequence of the patient derived HIV-1 protease and reverse transcriptase regions was determined using a fluorescence detection chain termination cycle sequencing methodology (ABI/PE). The method was used to determine a consensus nucleic acid sequence representing the combination of sequences of the mixture of HIV-1 variants existing in the subject sample (representing the quasispecies), and to determine the nucleic acid sequences of individual variants. Genotypes are analyzed as lists of amino acid differences between virus in the patient sample and a reference laboratory strain of HIV-1, NL4-3. Genotypes and corresponding phenotypes (fold-change in IC50 values) are entered in a relational database linking these two results with patient information. Large datasets can then be assembled from patient virus samples sharing particular characteristics, such as the presence of any given mutation, or combination of mutations or reduced susceptibility to any drug or combination of drugs.

(a) Protease inhibitor susceptibility of viruses containing mutations at amino acid 82 of HIV-1 Protease.

30

35

Phenotypic susceptibility profiles of 75 patient virus samples which contained a mutation at position 82 (V82A, F, S, or T), but no other primary mutations, were analyzed. According to most published guidelines, such viruses are expected to be resistant to ritonavir, nelfinavir, indinavir, and saquinavir. However, 8%, 20%, 23%, and 73% of these samples were phenotypically susceptible to these four protease inhibitors,

5 respectively (see Table 6). Thus, particularly for
indinavir and saquinavir, there was poor correlation
between the presence of mutations at position 82 and drug
susceptibility.

10 **(b) Indinavir susceptibility of viruses containing
combinations of mutations at amino acid 82 and one
secondary mutation in HIV-1 Protease.**

Indinavir resistance in viruses containing mutations at
position 82 was evaluated with respect to the presence of
15 other specific mutations. Decreased indinavir
susceptibility (fold-change in IC_{50} greater than 2.5) in
viruses containing V82A, F, S, or T but no other primary
mutations was correlated with the presence of mutations at
secondary positions. Reduced indinavir susceptibility was
20 observed in 20 samples containing mutations at both
positions 24 and 82 (100%) and in 27 samples with both 71
and 82 (100%) (See Table 7). The combination of mutations
at position 82 with mutations at other positions (e.g. 54,
46, 10, and 63) also significantly increased the
25 proportion of samples that had reduced indinavir
susceptibility (Table 7).

30 **(c) Saquinavir susceptibility of viruses containing
combinations of mutations at amino acid 82 and one
secondary mutation in HIV-1 Protease.**

Saquinavir resistance in viruses containing mutations at
position 82 was evaluated with respect to the presence of
other specific mutations. Decreased saquinavir
susceptibility (fold-change in IC_{50} greater than 2.5) in
35 viruses containing V82A, F, S, or T but no other primary
mutations was correlated with the presence of mutations at

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5 secondary positions. Reduced saquinavir susceptibility was
observed in 4 of 5 samples containing mutations at both
positions 20 and 82 (80%) and in 8 of 11 samples with both
36 and 82 (73%) (See Table 8). The combination of
10 mutations at position 82 with mutations at other positions
(e.g. 24, 71, 54, and 10) also significantly increased the
proportion of samples that had reduced saquinavir
susceptibility (Table 8).

**(d) Indinavir susceptibility of viruses containing
15 combinations of mutations at amino acid 82 and many
secondary mutations in HIV-1 Protease.**

Indinavir resistance in viruses containing mutations at
position 82 was evaluated with respect to the presence of
a defined number of other mutations. Decreased indinavir
20 susceptibility (fold-change in IC_{50} greater than 2.5) in
viruses containing V82A, F, S, or T but no other primary
mutations was correlated with the number of mutations at
secondary positions. Reduced indinavir susceptibility was
observed in 100% of samples with V82A, F, S, or T and at
25 least 6 other secondary mutations (See Table 9). The
proportion of samples that had reduced indinavir
susceptibility increased significantly in samples with
V82A, F, S, or T combined with 3 to 5 other secondary
mutations (Table 9).

30

**(e) Saquinavir susceptibility of viruses containing
combinations of mutations at amino acid 82 and many
secondary mutations in HIV-1 Protease.**

Saquinavir resistance in viruses containing mutations at
35 position 82 was evaluated with respect to the presence of
a defined number of other mutations. Decreased saquinavir

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5 susceptibility (fold-change in IC_{50} greater than 2.5) in
viruses containing V82A, F, S, or T but no other primary
mutations was correlated with the number of mutations at
secondary positions. Reduced saquinavir susceptibility
was observed in 60 to 76% of samples with V82A, F, S, or T
10 and at least 5 other secondary mutations (See Table 9).
The proportion of samples that had reduced saquinivir
susceptibility increased significantly in samples with
V82A, F, S, or T combined with 3 or 4 other secondary
mutations (Table 9).

EXAMPLE 8

Predicting Response to Protease Inhibitors by Characterization of Amino Acid 90 of HIV-1 Protease.

20 In one embodiment of this invention, changes in the amino
acid at position 90 of the protease protein of HIV-1 are
evaluated using the following method comprising: (i)
collecting a biological sample from an HIV-1 infected
25 subject; (ii) evaluating whether the biological sample
contains nucleic acid encoding HIV-1 protease having a
leucine to methionine (L90M) substitution at codon 90; and
(iii) determining susceptibility to protease inhibitors
(PRI).

30 The biological sample comprises whole blood, blood
components including peripheral mononuclear cells (PBMC),
serum, plasma (prepared using various anticoagulants such
as EDTA, acid citrate-dextrose, heparin), tissue biopsies,
35 cerebral spinal fluid (CSF), or other cell, tissue or body
fluids. In another embodiment, the HIV-1 nucleic acid

5 (genomic RNA) or reverse transcriptase protein can be
isolated directly from the biological sample or after
purification of virus particles from the biological
sample. Evaluating whether the amino acid at position 90
of the HIV-1 protease is mutated to methionine, can be
10 performed using various methods, such as direct
characterization of the viral nucleic acid encoding
protease or direct characterization of the protease
protein itself. Defining the amino acid at position 90 of
protease can be performed by direct characterization of
15 the protease protein by conventional or novel amino acid
sequencing methodologies, epitope recognition by
antibodies or other specific binding proteins or
compounds. Alternatively, the amino acid at position 90
of the HIV-1 protease protein can be defined by
20 characterizing amplified copies of HIV-1 nucleic acid
encoding the protease protein. Amplification of the HIV-1
nucleic acid can be performed using a variety of
methodologies including reverse transcription-polymerase
chain reaction (RT-PCR), NASBA, SDA, RCR, or 3SR. The
25 nucleic acid sequence encoding HIV protease at codon 90
can be determined by direct nucleic acid sequencing using
various primer extension-chain termination (Sanger, ABI/PE
and Visible Genetics) or chain cleavage (Maxam and
Gilbert) methodologies or more recently developed
30 sequencing methods such as matrix assisted laser
desorption-ionization time of flight (MALDI-TOF) or mass
spectrometry (Sequenom, Gene Trace Systems).
Alternatively, the nucleic acid sequence encoding amino
acid position 90 can be evaluated using a variety of probe
35 hybridization methodologies, such as genechip
hybridization sequencing (Affymetrix), line probe assay

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5 (LiPA; Murex), and differential hybridization (Chiron).

10 In a preferred embodiment of this invention, evaluation of
protease inhibitor susceptibility and of whether amino
acid position 90 of HIV-1 protease was wild type or
methionine, was carried out using a phenotypic
susceptibility assay or genotypic assay, respectively,
using resistance test vector DNA prepared from the
biological sample. In one embodiment, the plasma sample
was collected, viral RNA was purified and an RT-PCR
15 methodology was used to amplify a patient derived segment
encoding the HIV-1 protease and reverse transcriptase
regions. The amplified patient derived segments were then
incorporated, via DNA ligation and bacterial
transformation, into an indicator gene viral vector
20 thereby generating a resistance test vector. Resistance
test vector DNA was isolated from the bacterial culture
and the phenotypic susceptibility assay was carried out
and analyzed as described in Example 1.

25 The nucleic acid (DNA) sequence of the patient derived
HIV-1 protease and reverse transcriptase regions was
determined using a fluorescence detection chain
termination cycle sequencing methodology (ABI/PE). The
method was used to determine a consensus nucleic acid
30 sequence representing the combination of sequences of the
mixture of HIV-1 variants existing in the subject sample
(representing the quasispecies), and to determine the
nucleic acid sequences of individual variants. Genotypes
are analyzed as lists of amino acid differences between
35 virus in the patient sample and a reference laboratory
strain of HIV-1, NL4-3. Genotypes and corresponding

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5 phenotypes (fold-change in IC₅₀ values) are entered in a
relational database linking these two results with patient
information. Large datasets can then be assembled from
patient virus samples sharing particular characteristics,
such as the presence of any given mutation, or combination
10 of mutants, or reduced susceptibility to any drug or
combination of drugs.

**(a) Protease inhibitor susceptibility of viruses
containing mutations at amino acid 90 of HIV-1 Protease.**

15 Phenotypic susceptibility profiles of 58 patient virus
samples which contained a mutation at position 90 (L90M),
but no other primary mutations, were analyzed. According
to most published guidelines, such viruses are expected to
be resistant to ritonavir, nelfinavir, indinavir, and
20 saquinavir. However, 28%, 9%, 31%, and 47% of these
samples were phenotypically susceptible to these four
protease inhibitors, respectively (see Table 6). Thus,
particularly for indinavir and saquinavir, there was poor
25 correlation between the presence of mutations at position
90 and drug susceptibility.

**(b) Indinavir susceptibility of viruses containing
combinations of mutations at amino acid 90 and one
30 secondary mutation in HIV-1 Protease.**

Indinavir resistance in viruses containing mutations at
position 90 was evaluated with respect to the presence of
other specific mutations. Decreased indinavir
susceptibility (fold-change in IC₅₀ greater than 2.5) in
35 viruses containing L90M but no other primary mutations was
correlated with the presence of mutations at secondary

5 positions. Reduced indinavir susceptibility was observed
in 17 of 19 samples containing mutations at both positions
73 and 90 (89%) and in 16 of 18 samples with both 71 and
90 (89%) (See Table 10). The combination of mutations at
10 position 90 with mutation at position 46 also
significantly increased the proportion of samples that had
reduced indinavir susceptibility (Table 10).

(c) Saquinavir susceptibility of viruses containing combinations of mutations at amino acid 90 and one secondary mutation in HIV-1 Protease.

15 Saquinavir resistance in viruses containing mutations at
position 90 was evaluated with respect to the presence of
other specific mutations. Decreased saquinavir
susceptibility (fold-change in IC_{50} greater than 2.5) in
20 viruses containing L90M but no other primary mutations was
correlated with the presence of mutations at secondary
positions. Reduced saquinavir susceptibility was observed
in 15 of 19 samples containing mutations at both positions
73 and 90 (79%) and in 14 of 18 samples with both 71 and
25 90 (78%) (See Table 11). The combination of mutations at
position 90 with mutations at other positions (e.g. 77 and
10) also significantly increased the proportion of samples
that had reduced saquinavir susceptibility (Table 1).

30

(d) Indinavir susceptibility of viruses containing combinations of mutations at amino acid 90 and many secondary mutations in HIV-1 Protease.

35 Indinavir resistance in viruses containing mutations at

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5 position 90 was evaluated with respect to the presence of
a defined number of other mutations. Decreased indinavir
susceptibility (fold-change in IC_{50} greater than 2.5) in
viruses containing L90M but no other primary mutations was
correlated with the number of mutations at secondary
10 positions. Reduced indinavir susceptibility was observed
in 100% of samples with L90M and at least 5 other
secondary mutations had (See Table 12). The proportion of
samples that had reduced indinavir susceptibility
increased significantly in samples with L90M combined with
15 3 or 4 other secondary mutations (Table 12).

(e) Saquinavir susceptibility of viruses containing combinations of mutations at amino acid 90 and many secondary mutations in HIV-1 Protease.

20 Saquinavir resistance in viruses containing mutations at
position 90 was evaluated with respect to the presence of
a defined number of other mutations. Decreased saquinavir
susceptibility (fold-change in IC_{50} greater than 2.5) in
viruses containing L90M but no other primary mutations was
25 correlated with the number of mutations at secondary
positions. Reduced saquinavir susceptibility was observed
in 100% of samples with L90M and at least 5 other
secondary mutations (See Table 12). The proportion of
samples that had reduced saquinavir susceptibility
30 increased significantly in samples with L90M combined with
3 or 4 other secondary mutations (Table 12).

EXAMPLE 9

**Predicting Response to Protease Inhibitors by
35 Characterization of Amino Acids 82 and 90 of HIV-1
Protease.**

5

In one embodiment of this invention, changes in the amino acid at position 82 and 90 of the protease protein of HIV-1 are evaluated using the following method comprising:

- 10 (i) collecting a biological sample from an HIV-1 infected subject; (ii) evaluating whether the biological sample contains nucleic acid encoding HIV-1 protease having a valine to alanine (V82A), phenylalanine (V82F), serine (V82S), or threonine (V82T) substitution at codon 82 or a leucine to methionine at position 90 (L90M); and (iii) 15 determining susceptibility to protease inhibitors (PRI).

The biological sample comprises whole blood, blood components including peripheral mononuclear cells (PBMC), serum, plasma (prepared using various anticoagulants such as EDTA, acid citrate-dextrose, heparin), tissue biopsies, 20 cerebral spinal fluid (CSF), or other cell, tissue or body fluids. In another embodiment, the HIV-1 nucleic acid (genomic RNA) or reverse transcriptase protein can be isolated directly from the biological sample or after 25 purification of virus particles from the biological sample. Evaluating whether the amino acid at position 82 of the HIV-1 protease is mutated to alanine, phenylalanine, serine, or threonine or at position 90 to methionine, can be performed using various methods, such as direct characterization of the viral nucleic acid 30 encoding protease or direct characterization of the protease protein itself. Defining the amino acid at positions 82 and 90 of protease can be performed by direct characterization of the protease protein by conventional or novel amino acid sequencing methodologies, epitope 35 recognition by antibodies or other specific binding

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5 proteins or compounds. Alternatively, the amino acid at
positions 82 and 90 of the HIV-1 protease protein can be
defined by characterizing amplified copies of HIV-1
nucleic acid encoding the protease protein. Amplification
of the HIV-1 nucleic acid can be performed using a variety
10 of methodologies including reverse
transcription-polymerase chain reaction (RT-PCR), NASBA,
SDA, RCR, or 3SR. The nucleic acid sequence encoding HIV
protease at codons 82 and 90 can be determined by direct
nucleic acid sequencing using various primer
15 extension-chain termination (Sanger, ABI/PE and Visible
Genetics) or chain cleavage (Maxam and Gilbert)
methodologies or more recently developed sequencing
methods such as matrix assisted laser
desorption-ionization time of flight (MALDI-TOF) or mass
20 spectrometry (Sequenom, Gene Trace Systems).
Alternatively, the nucleic acid sequence encoding amino
acid positions 82 and 90 can be evaluated using a variety
of probe hybridization methodologies, such as genechip
hybridization sequencing (Affymetrix), line probe assay
25 (LiPA; Murex), and differential hybridization (Chiron).

In a preferred embodiment of this invention, evaluation of
protease inhibitor susceptibility and of whether amino
acid positions 82 and 90 of HIV-1 protease was wild type
30 or alanine, phenylalanine, serine, or threonine in the
case of position 82 and methionine at position 90, was
carried out using a phenotypic susceptibility assay or
genotypic assay, respectively, using resistance test
vector DNA prepared from the biological sample. In one
35 embodiment, plasma sample was collected, viral RNA was
purified and an RT-PCR methodology was used to amplify a

5 patient derived segment encoding the HIV-1 protease and
reverse transcriptase regions. The amplified patient
derived segments were then incorporated, via DNA ligation
and bacterial transformation, into an indicator gene viral
10 Resistance test vector DNA was isolated from the bacterial
culture and the phenotypic susceptibility assay was
carried out and analyzed as described in Example 1.

15 The nucleic acid (DNA) sequence of the patient derived
HIV-1 protease and reverse transcriptase regions was
determined using a fluorescence detection chain
termination cycle sequencing methodology (ABI/PE). The
method was used to determine a consensus nucleic acid
sequence representing the combination of sequences of the
20 mixture of HIV-1 variants existing in the subject sample
(representing the quasispecies), and to determine the
nucleic acid sequences of individual variants. Genotypes
are analyzed as lists of amino acid differences between
virus in the patient sample and a reference laboratory
25 strain of HIV-1, NL4-3. Genotypes and corresponding
phenotypes (fold-change in IC50 values) are entered in a
relational database linking these two results with patient
information. Large datasets can then be assembled from
patient virus samples sharing particular characteristics,
30 such as the presence of any given mutation or reduced
susceptibility to any drug or combination of drugs.

**Protease inhibitor susceptibility of viruses containing
mutations at amino acids 82 and 90 of HIV-1 Protease.**

35 Phenotypic susceptibility profiles of 33 patient virus
samples which contained mutations at positions 82 (V82A,

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5 F, S, or T) and 90 (L90M), but no other primary mutations,
were analyzed. According to most published guidelines,
such viruses are expected to be resistant to ritonavir,
nelfinavir, indinavir, and saquinavir. However, 9% and
21% of these samples were phenotypically susceptible to
10 indinavir and saquinavir, respectively (see Table 6).
Thus, particularly for saquinavir, there was poor
correlation between the presence of mutations at positions
82 and 90 and drug susceptibility.

EXAMPLE 10

Measuring Replication Fitness Using Resistance Test 20 Vectors

^ A means and method is provided for accurately measuring
and reproducing the replication fitness of HIV-1. This
method for measuring replication fitness is applicable to
25 other viruses, including, but not limited to
hepadnaviruses (human hepatitis B virus), flaviviruses
(human hepatitis C virus) and herpesviruses (human
cytomegalovirus). This example further provides a means
and method for measuring the replication fitness of HIV-1
30 that exhibits reduced drug susceptibility to reverse
transcriptase inhibitors and protease inhibitors. This
method can be used for measuring replication fitness for
other classes of inhibitors of HIV-1 replication,
including, but not limited to integration, virus assembly,
35 and virus attachment and entry.

5 Replication fitness tests are carried out using the means
and methods for phenotypic drug susceptibility and
resistance tests described in US Patent Number 5,837,464
(International Publication Number WO 97/27319) which is
hereby incorporated by reference.

10

In these experiments patient-derived segment(s)
corresponding to the HIV protease and reverse
transcriptase coding regions were either patient-derived
segments amplified by the reverse transcription-polymerase
15 chain reaction method (RT-PCR) using viral RNA isolated
from viral particles present in the serum of HIV-infected
individuals or were mutants of wild type HIV-1 made by
site directed mutagenesis of a parental clone of
resistance test vector DNA. Resistance test vectors are
20 also referred to as "fitness test vectors" when used to
evaluate replication fitness. Isolation of viral RNA was
performed using standard procedures (e.g. RNeasy Total
RNA Isolation System, Promega, Madison WI or RNeasy,
Tel-Test, Friendswood, TX). The RT-PCR protocol was
25 divided into two steps. A retroviral reverse
transcriptase [e.g. Moloney MuLV reverse transcriptase
(Roche Molecular Systems, Inc., Branchburg, NJ), or avian
myeloblastosis virus (AMV) reverse transcriptase,
(Boehringer Mannheim, Indianapolis, IN)] was used to copy
30 viral RNA into cDNA. The cDNA was then amplified using a
thermostable DNA polymerase [e.g. Taq (Roche Molecular
Systems, Inc., Branchburg, NJ), Tth (Roche Molecular
Systems, Inc., Branchburg, NJ), PrimeZyme (isolated from
Thermus brockianus, Biometra, Gottingen, Germany)] or a
35 combination of thermostable polymerases as described for
the performance of "long PCR" (Barnes, W.M., (1994) Proc.

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5 Natl. Acad. Sci, USA 91, 2216-2220) [e.g. Expand High Fidelity PCR System (Taq + Pwo), (Boehringer Mannheim. Indianapolis, IN) OR GeneAmp XL PCR kit (Tth + Vent), (Roche Molecular Systems, Inc., Branchburg, NJ)].

10 PCR6 (Table 5, #1) is used for reverse transcription of viral RNA into cDNA. The primers, ApaI primer (PDSApa, Table 5, #2) and AgeI primer (PDSAge, Table 5, #3) used to amplify the "test" patient-derived segments contained sequences resulting in ApaI and AgeI recognition sites
15 being introduced into both ends of the PCR product, respectively.

20 Fitness test vectors incorporating the "test" patient-derived segments were constructed as described in US Patent Number 5,837,464 (International Publication Number WO/97/27319) (see Fig. 1) using an amplified DNA product of 1.5 kB prepared by RT-PCR using viral RNA as a template and oligonucleotides PCR6 (#1), PDSApa (#2) and
25 PDSAge (#3) as primers, followed by digestion with ApaI and AgeI or the isoschizomer PinA1. To ensure that the plasmid DNA corresponding to the resultant fitness test vector comprises a representative sample of the HIV viral quasi-species present in the serum of a given patient,
30 many (>100) independent E. coli transformants obtained in the construction of a given fitness test vector were pooled and used for the preparation of plasmid DNA.

35 A packaging expression vector encoding an amphotrophic MuLV 4070A env gene product enables production in a fitness test vector host cell of fitness test vector viral

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5 particles which can efficiently infect human target cells.
Fitness test vectors encoding all HIV genes with the
exception of env were used to transfect a packaging host
cell (once transfected the host cell is referred to as a
fitness test vector host cell). The packaging expression
10 vector which encodes the amphotrophic MuLV 4070A env gene
product is used with the resistance test vector to enable
production in the fitness test vector host cell of
infectious pseudotyped fitness test vector viral
particles.

15 Fitness tests performed with fitness test vectors were
carried out using packaging host and target host cells
consisting of the human embryonic kidney cell line 293
(Cell Culture Facility, UC San Francisco, SF, CA)..

20 Fitness tests were carried out with fitness test vectors
using two host cell types. Fitness test vector viral
particles were produced by a first host cell (the fitness
test vector host cell) that was prepared by transfecting a
25 packaging host cell with the fitness test vector and the
packaging expression vector. The fitness test vector
viral particles were then used to infect a second host
cell (the target host cell) in which the expression of the
indicator gene is measured (see Fig. A).

30 The fitness test vectors containing a functional
luciferase gene cassette were constructed and host cells
were transfected with the fitness test vector DNA. The
fitness test vectors contained patient-derived reverse
35 transcriptase and protease DNA sequences that encode
proteins which were either susceptible or resistant to the

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5 antiretroviral agents, such as nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors and protease inhibitors._

10 The amount of luciferase activity detected in the infected cells is used as a direct measure of "infectivity", "replication capacity" or "fitness", i.e. the ability of the virus to complete a single round of replication. Relative fitness is assessed by comparing the amount of luciferase activity produced by patient derived viruses to
15 the amount of luciferase activity produced by a well-characterized reference virus (wildtype) derived from a molecular clone of HIV-1, for example NL4-3 or HXB2. Fitness measurements are expressed as a percent of the reference, for example 25%, 50%, 75%, 100% or 125% of
20 reference (Figure B, C).

25 Host cells were seeded in 10⁻⁶cm-diameter dishes and were transfected one day after plating with fitness test vector plasmid DNA and the envelope expression vector. Transfections were performed using a calcium-phosphate co-precipitation procedure. The cell culture media containing the DNA precipitate was replaced with fresh medium, from one to 24 hours, after transfection. Cell culture media containing fitness test vector viral
30 particles was harvested one to four days after transfection and was passed through a 0.45-mm filter before being stored at -80°C. HIV capsid protein (p24) levels in the harvested cell culture media were determined by an EIA method as described by the manufacturer (SIAC; Frederick, MD). Before infection, target cells (293 and
35 293/T) were plated in cell culture media. Control

5 infections were performed using cell culture media from
mock transfections (no DNA) or transfections containing
the fitness test vector plasmid DNA without the envelope
expression plasmid. One to three or more days after
10 infection the media was removed and cell lysis buffer
(Promega) was added to each well. Cell lysates were
assayed for luciferase activity. Alternatively, cells
were lysed and luciferase was measured by adding Steady-
Glo (Promega) reagent directly to each well without
aspirating the culture media from the well.

15 **Example 11**

**Measuring Replication Fitness of Viruses with
Deficiencies in Reverse Transcriptase Activity**

20 A means and method is provided for identifying mutations
in reverse transcriptase that alter replication fitness.
A means and method is provided for identifying mutations
that alter replication fitness and can be used to identify
mutations associated with other aspects of HIV-1
25 replication, including, but not limited to integration,
virus assembly, and virus attachment and entry. This
example also provides a means and method for quantifying
the affect that specific mutations reverse transcriptase
have on replication fitness. A means and method for
30 quantifying the affect that specfic protease and reverse
transcriptase mutations have on replication fitness to
mutations in other viral genes involved in HIV-1
replication, including, but not limited to the gag, pol,
and envelope genes is also provided.

35

Fitness test vectors were constructed as described in

5 example 10. Fitness test vectors derived from patient
samples or clones derived from the fitness test vector
pools, or fitness test vectors were engineered by site
directed mutagenesis to contain specific mutations, and
were tested in a fitness assay to determine accurately and
10 quantitatively the relative fitness compared to a well-
characterized reference standard. A patient sample was
examined for increased or decreased reverse transcriptase
activity and correlated with the relative fitness observed
(Figure C).

15 **Reverse transcriptase activity of patient HIV samples**

Reverse transcriptase activity can be measured by any
number of widely used assay procedures, including but not
limited to homopolymeric extension using (e.g. oligo
dT:poly rC) or real time PCR based on molecular beacons
20 (reference Kramer) or 5' exonuclease activity (Lie and
Petropoulos, 1996). In one embodiment, virion associated
reverse transcriptase activity was measured using a
quantitative PCR assay that detects the 5' exonuclease
activity associated with thermo-stable DNA polymerases
25 (Figure C). In one embodiment of the invention, the
fitness of the patient virus was compared to a reference
virus to determine the relative fitness compared to
"wildtype" viruses that have not been exposed to reverse
transcriptase inhibitor drugs. In another embodiment, the
30 fitness of the patient virus was compared to viruses
collected from the same patient at different timepoints,
for example prior to initiating therapy, before or after
changes in drug treatment, or before or after changes in
virologic (RNA copy number), immunologic (CD4 T-cells), or
35 clinical (opportunistic infection) markers of disease
progression.

5

Genotypic analysis of patient HIV samples

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10 Fitness test vector DNAs, either pools or clones, are analyzed by any of the genotyping methods described in Example 1. In one embodiment of the invention, patient HIV sample sequences were determined using viral RNA purification, RT/PCR and ABI chain terminator automated sequencing. The sequence was determined and compared to reference sequences present in the database or compared to a sample from the patient prior to initiation of therapy.
15 The genotype was examined for sequences that are different from the reference or pre-treatment sequence and correlated to the observed fitness.

Fitness analysis of site directed mutants

20 Genotypic changes that are observed to correlate with changes in fitness were evaluated by construction of fitness vectors containing the specific mutation on a defined, wild-type (drug susceptible) genetic background.
25 Mutations may be incorporated alone and/or in combination with other mutations that are thought to modulate the fitness of a virus. Mutations were introduced into the fitness test vector through any of the widely known methods for site-directed mutagenesis. In one embodiment
30 of this invention the mega-primer PCR method for site-directed mutagenesis is used. A fitness test vector containing the specific mutation or group of mutations were then tested using the fitness assay described in Example 10 and the fitness was compared to that of a
35 genetically defined wild-type (drug susceptible) fitness test vector which lacks the specific mutations. Observed

5 changes in fitness are attributed to the specific
mutations introduced into the resistance test vector. In
several related embodiments of the invention, fitness test
vectors containing site directed mutations in reverse
10 transcriptase that result in amino acid substitutions at
position 190 (G190A, G190S, G190C, G190E, G190V, G190T)
and that display different amounts of reverse
transcriptase activity were constructed and tested for
fitness (Figure D). The fitness results were correlated
with specific reverse transcriptase amino acid
15 substituions and fitness.

Example 12

Measuring Replication Fitness of Viruses with Deficiencies in Protease Activity

20

A means and method for identifying mutations in protease
that alter replication fitness is provided.

This example provides the means and methods for
25 identifying mutations that alter replication fitness for
various components of HIV-1 replication, including, but
not limited to integration, virus assembly, and virus
attachment and entry. This example also provides a means
and method for quantifying the affect that specific
30 mutations in protease or reverse transcriptase have on
replication fitness. This method can be used for
quantifying the effect that specific protease mutations
have on replication fitness and can be used to quantify
the effect of other mutations in other viral genes
35 involved in HIV-1 replication, including, but not limited
to the gag, pol, and envelope genes.

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15

Fitness test vectors were constructed as described in example 10. Fitness test vectors derived from patient samples or clones derived from the fitness test vector pools, or fitness test vectors engineered by site directed mutagenesis to contain specific mutations, were tested in a fitness assay to determine accurately and quantitatively the relative fitness compared to a well-characterized reference standard. A patient sample was examined further for increased or decreased protease activity correlated with the relative fitness observed (Figure C).

20

25

30

35

Protease activity of patient HIV samples

Protease activity can be measured by any number of widely used assay procedures, including but not limited to in vitro reactions that measure protease cleavage activity (reference Erickson). In one embodiment, protease cleavage of the gag polyprotein (p55) was measured by Western blot analysis using an anti-capsid (p24) antibody (Figure C). In one embodiment of the invention, the fitness of the patient virus was compared to a reference virus to determine the relative fitness compared to "wildtype" viruses that have not been exposed to protease inhibitor drugs. In another embodiment, the fitness of the patient virus was compared to viruses collected from the same patient at different timepoints, for example prior to initiating therapy, before or after changes in drug treatment, or before or after changes in virologic (RNA copy number), immunologic (CD4 T-cells), or clinical (opportunistic infection) markers of disease progression.

Genotypic analysis of patient HIV samples

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5 Fitness test vector DNAs, either pools or clones, are
analyzed by any of the genotyping methods described in
Example 1. In one embodiment of the invention, patient
HIV sample sequences were determined using viral RNA
purification, RT/PCR and ABI chain terminator automated
10 sequencing. The sequence was determined and compared to
reference sequences present in the database or compared to
a sample from the patient prior to initiation of therapy,
if available. The genotype was examined for sequences
that are different from the reference or pre-treatment
15 sequence and correlated to the observed fitness.

Fitness analysis of site directed mutants

Genotypic changes that are observed to correlate with
20 changes in fitness are evaluated by construction of
fitness vectors containing the specific mutation on a
defined, wild-type (drug susceptible) genetic background.
Mutations may be incorporated alone and/or in combination
with other mutations that are thought to modulate the
25 fitness of a virus. Mutations are introduced into the
fitness test vector through any of the widely known
methods for site-directed mutagenesis. In one embodiment
of this invention the mega-primer PCR method for
site-directed mutagenesis is used. A fitness test vector
30 containing the specific mutation or group of mutations are
then tested using the fitness assay described in Example
10 and the fitness is compared to that of a genetically
defined wild-type (drug susceptible) fitness test vector
which lacks the specific mutations. Observed changes in
35 fitness are attributed to the specific mutations
introduced into the fitness test vector. In several

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5 related embodiments of the invention, fitness test vectors
containing site directed mutations in reverse protease
that result in amino acid substitutions at positions 30,
63, 77, 90 (list from Figure E) and that display different
amounts of protease activity are constructed and tested
10 for fitness (Figure E). The fitness results enable the
correlation between specific protease amino acid
substitutions and changes in viral fitness.

Example 13

15 **Measuring Replication Fitness and Drug Susceptibility in a Large Patient Population**

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20 This example describes the high incidence of patient
samples with reduced replication fitness. This example
also describes the general correlation between reduced
drug susceptibility and reduced replication fitness. This
example further describes the occurrence of viruses with
reduced fitness in patients receiving protease inhibitor
and/or reverse transcriptase inhibitor treatment. This
25 example further describes the incidence of patient samples
with reduced replication fitness in which the reduction in
fitness is due to altered protease processing of the gag
polyprotein (p55). This example further describes the
incidence of protease mutations in patient samples that
30 exhibit low, moderate or normal (wildtype) replication
fitness. This example further describes protease mutations
that are frequently observed, either alone or in
combination, in viruses that exhibit reduced replication
capacity. This example also describes the incidence of
35 patient samples with reduced replication fitness in which
the reduction in fitness is due to altered reverse

5 transcriptase activity. This example describes the
occurrence of viruses with reduced replication fitness in
patients failing antiretroviral drug treatment.

10 Fitness/resistance test vectors were constructed as
described in example 10. Fitness and drug susceptibility
was measured in 134 random patient samples that were
received for routing phenotypic testing by the ViroLogic
Clinical Reference Laboratory. Fitness assays were
15 performed as described in Example 10. Drug susceptibility
testing and genotyping of the protease region was
performed as described in Example 1. Reverse
transcriptase activity was measured as described in
Example 11. Protease processing was measured as described
in Example 12.

20

Drug susceptibility of patient viruses

Reduced drug susceptibility was observed for a majority of
the patient virus samples (Table A). 66 percent of the
viruses exhibited large (define as >10X of the reference)
25 reductions in susceptibility to one or more NRTI drugs.
52 percent of the viruses exhibited large reductions in
susceptibility to one or more NNRTI drugs. 45 percent of
the viruses exhibited large reductions in susceptibility
to one or more PRI drugs.

30

Fitness of patient viruses

Reduced replication fitness was observed for a majority of
the patient virus samples (Table A). Forty one percent of
the viruses exhibited large reductions in replication
35 fitness (<25% of the reference). Another 45% had moderate
reductions (between 25-75% of the reference) in

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5 replication fitness. A minority of the patient samples
(14%) displayed replication fitness that approached or
exceeded "wildtype" levels (>75% of the reference).
Viruses with reduced drug susceptibility, were much more
likely to display reduced replication fitness (Figures F,
10 G, H, and I).

Protease Mutations in patient viruses

Greater than 10 mutations in protease were observed in a
majority of the patient virus samples (Table A). Viruses
15 with reduced fitness were much more likely to contain 10
or more protease mutations (Figure I). Sixty two percent
of the viruses that exhibited large reductions in
replication fitness (<25% of the reference) contained 10
or more protease mutations. Twenty two percent of the
20 viruses with moderate reductions (between 25-75% of the
reference) in fitness contained 10 or more protease
mutations. Only 5% of the viruses that displayed
replication fitness that approached or exceeded "wildtype"
levels (>75% of the reference) contained 10 or more
25 protease mutations (Table A). Certain protease mutations
either alone (D30N) or in combination (L90M plus K20T, or
M46I, or 73, or N88D) were observed at high incidences in
viruses with reduced fitness (Figures I and J).

Protease processing of patient viruses

30 Reduced protease processing of the p55 gag polyprotein was
observed in a majority of the patient virus samples (Table
A). Viruses with reduced fitness were much more likely to
display reduced protease processing; defined as having

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5 detectable amounts of the p41 intermediate cleavage
product (Figures F, I and K). Seventy one percent of the
viruses that exhibited large reductions in replication
fitness (<25% of the reference) displayed reduced protease
processing. Eighteen percent of the viruses with moderate
10 fitness reductions (between 25-75% of the reference)
displayed reduced protease processing. Only 10% of the
viruses that displayed replication fitness that approached
or exceeded "wildtype" levels (>75% of the reference)
exhibited reduced protease processing (Table A). Certain
15 protease mutations (D30N, M46I/L, G48V, I54L/A/S/T/V, and
I84V) were observed at high incidences in viruses with
reduced protease processing of the p55 gag polyprotein
(Figure L).

20 **Reverse transcriptase of patient viruses**

Reduced reverse transcriptase activity processing was
observed in a minority of the patient virus samples (Table
A). Viruses with reduced fitness were much more likely to
display reduced reverse transcriptase activity. Fourteen
25 percent of the viruses that exhibited large reductions in
replication fitness (<25% of the reference) displayed
reduced reverse transcriptase activity. Only 2% of the
viruses with moderate fitness reductions (between 25-75%
of the reference) displayed reduced reverse transcriptase
30 activity. None of the viruses that displayed replication
fitness that approached or exceeded "wildtype" levels
(>75% of the reference) exhibited reduced reverse
transcriptase activity.

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5

Example 14

Measuring Replication Fitness to Guide Treatment Decisions

10 A means and method for using replication fitness
measurements to guide the treatment of HIV-1 is provided.
This example further provides a means and method for using
replication fitness measurements to guide the treatment of
patients failing antiretroviral drug treatment. This
example further provides the means and methods for using
replication fitness measurements to guide the treatment of
15 patients newly infected with HIV-1.

**Guiding treatment of patients with multi-drug resistant
virus:** Fitness/resistance test vectors were constructed as
described in example 10. Fitness and drug susceptibility
20 were measured on serial longitudinal samples collected
weekly for 12 weeks from 18 patients. These patients were
considered failing a protease inhibitor (typically
indinavir) containing regimen and had incomplete
suppression of virus replication based on routine viral
25 load testing (>2,500 copies/mL). Phenotypic drug
susceptibility testing indicated that these patient
viruses were multi-drug resistant. Each patient agreed to
interrupt therapy for a period of at least 12 weeks.
Phenotypic drug susceptibility assays were performed as
30 described in Example 1 on serial samples collected just
prior to interrupting therapy and weekly during the period
of interruption. Fitness assays were performed as
described in Example 10 on serial samples collected just
prior to interrupting therapy and weekly during the period

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5 of interruption. Protease processing was measured as described in Example 12.

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10 Of the 18 patients that interrupted therapy, 16 patients had resistant viruses that regained susceptibility to antiretroviral drugs during the period of treatment interruption. The phenotypic test results of a representative patient are shown in Figure M. Typically, susceptibility returned to all drug classes simultaneously, consistent with the re-emergence of a
15 minor population of drug sensitive virus. In the representative example shown in Figure M, drug sensitivity was abruptly restored between weeks 9 and 10. Genotypic analysis (DNA sequence of protease and reverse transcriptase) are also consistent with the re-emergence
20 of a drug sensitive virus. These data show the loss of most or all drug resistance mutation simultaneously (data not shown). The data are not consistent with random back mutations. Back mutations would predict that restored susceptibility to drugs would occur unevenly for different
25 drug classes and/or within a drugs within the same class.

Generally, the re-emergence of the drug susceptible virus was also accompanied by a simultaneous increase in replication fitness. This relationship is clearly evident
30 for the representative virus (Figure N). Several other examples with less frequent timepoints are shown in Figure O. Virus from patients that did not revert to drug susceptibility after interruption generally did not exhibit an increase in replication fitness, nor did

5 viruses from patients that did not interrupt treatment
(Figures 0). The data indicate that the drug sensitive
virus that re-emerged after treatment interruption is able
to replicate better than the drug resistant virus that was
present before treatment was interrupted. The re-
10 emergence of drug susceptible virus in this group of
patients was also accompanied by an increase in viral load
and a decrease in DC4 T-cells, indicators of disease
progression. Thus, fitness information can be used to
guide treatment of patients that harbor multi-drug
15 resistant virus and are considering treatment
interruption. If the patient virus is drug resistant but
has low replication capacity, the patient and the
physician should consider continuing drug treatment to
prevent the re-emergence of a drug sensitive virus with
20 higher replication capacity and greater pathogenecity.
Alternatively, if the patient virus is drug resistant and
has high replication capacity, the patient and the
physician may consider interrupting treatment to spare the
patient from the harmful and unpleasant side effects of
25 antiretroviral drugs that are not providing clinical
benefit.

Furthermore, physicians may choose to perform routine
replication fitness assays for patients that have multi-
30 drug resistant virus. This assay could be used to monitor
the replication fitness of patient viruses when complete
suppression of virus replication is not possible due to
multi-drug resistance. The assay would be used to guide
treatment decisions that prevent the drug resistant virus

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5 with low replication fitness from increasing its
replication fitness. In this way, physicians may prolong
the usefulness of antiretroviral drugs despite the
presence of drug resistant virus in the patient.

10 **Guiding treatment of newly infected patients:**

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15 Patients that maintain high virus loads (setpoint) after
acute infection are more likely to exhibit accelerated
disease progression. Therefore, it is advantageous for
this class of patient to initiate antiretroviral drug
treatment as soon as possible after diagnosis with HIV-1
infection. In conjunction with viral load, fitness
measurements of viruses in newly infected patients may
provide a useful measurement to identify those individuals
20 that will develop elevated setpoints after primary
infection and consequently are likely to exhibit
accelerated disease progression. Fitness measurements may
guide the decision to treat immediately after diagnosis or
a some later time point.

25

Example 15

**Measuring Saquinavir Susceptibility of Viruses
Containing Various Amino Acid Substitutions in
Protease at Position 82**

30

This example provides a means and method for identifying
mutations in protease that affect susceptibility
(increased or decreased) to saquinavir.

5 In one embodiment of this invention, the effects of
combination of mutations at position 82 (for example,
V82A, V82F, V82S, or V82T are evaluated using the
following method comprising: (i)collecting a biological
10 whether the HIV-1 in the sample contains nucleic acid
encoding protease having a valine to alanine (V82A),
phenylalanine (V82F), serine (V82S), or threonine (V82T)
substitution at position 82 or a leucine to methionine
substitution at position 90 (L90M); and (iii) determining
15 susceptibility to protease inhibitors (PRIs).

The biological sample comprises whole blood, blood
components including peripheral mononuclear cells (PBMC),
serum, plasma (prepared using various anticoagulants such
20 as EDTA, acid citrate-dextrose, heparin), tissue biopsies,
cerebral spinal fluid (CSF), or other cell, tissue or body
fluids. In another embodiment, the HIV-1 nucleic acid
(genomic RNA) or reverse transcriptase protein can be
isolated directly from the biological sample or after
25 purification of virus particles from the biological
sample. Evaluating whether the amino acid at position 82
of the HIV-1 protease is mutated to alanine,
phenylalanine, or threonine, can be performed using
various methods, such as direct characterization of the
30 viral nucleic acid encoding protease or direct
characterization of the protease protein itself. Defining
the amino acid at position 82 of protease can be performed
by direct characterization of the protease protein by
conventional or novel amino acid sequencing methodologies,

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^

5 epitope recognition by antibodies or other specific
binding proteins or compounds. Alternatively, the amino
acid at position 82 of the HIV-1 protease protein can be
defined by characterizing amplified copies of HIV-1
10 nucleic acid encoding the protease protein. Amplification
of the HIV-1 nucleic acid can be performed using a variety
of methodologies including reverse
transcription-polymerase chain reaction (RT-PCR), NASBA,
SDA, RCR, or 3SR. The nucleic acid sequence encoding HIV
protease at codon 82 can be determined by direct nucleic
15 acid sequencing using various primer extension-chain
termination (Sanger, ABI/PE and Visible Genetics) or chain
cleavage (Maxam and Gilbert) methodologies or more
recently developed sequencing methods such as matrix
assisted laser desorption-ionization time of flight
20 (MALDI-TOF) or mass spectrometry (Sequenom, Gene Trace
Systems). Alternatively, the nucleic acid sequence
encoding amino acid position 82 can be evaluated using a
variety of probe hybridization methodologies, such as
genechip hybridization sequencing (Affymetrix), line probe
25 assay (LiPA; Murex), and differential hybridization
(Chiron).

30 In a preferred embodiment of this invention, evaluation of
the effects of mutations at amino acid position 82 of
HIV-1 protease on protease inhibitor susceptibility, was
carried out using a phenotypic susceptibility assay using
resistance test vector DNA prepared from the biological
sample. In one embodiment, plasma samples were collected,

5 viral RNA was purified and an RT-PCR methodology was used
to amplify a patient derived segment encoding the HIV-1
protease and reverse transcriptase regions. The amplified
patient derived segments were then incorporated, via DNA
ligation and bacterial transformation, into an indicator
10 gene viral vector thereby generating a resistance test
vector. Resistance test vector DNA was isolated from the
bacterial culture and the phenotypic susceptibility assay
was carried out as described in Example 1. The genotype of
the protease region was determined by dideoxy chain-
15 termination sequencing of the resistance test vector DNA.
The results are summarized for saquinavir (SQV) in Figure
6. Samples were categorized as having mutations in
protease encoding alanine (A), phenylalanine (F), or
threonine (T) at position 82, instead of the wild-type
20 valine (V), and the percentage of samples in each category
displaying hyper-sensitivity to saquinavir (i.e., fold-
change vs. reference of 0.4 or less) was determined.
Surprisingly, the percentage of saquinavir hyper-
susceptible viruses was much higher amongst viruses
25 containing V82F than those containing V82A or V82T. This
observation implies that the detection of V82F in protease
predicts a positive virological response to saquinavir
treatment.

5

Example 16

**Measuring Replication Fitness of Viruses with
Mutations in Integrase**

10 This example provides a means and method for identifying
mutations in integrase that alter replication fitness.

15 This example provides the means and methods for
identifying mutations that alter replication fitness for
various components of HIV-1 replication, including, but
not limited to integration, virus assembly, and virus
attachment and entry. This example also provides a means
and method for quantifying the affect that specific
20 mutations in protease, reverse transcriptase, or integrase
have on replication fitness. This method can be used for
quantifying the effect that specific integrase mutations
have on replication fitness and can be used to quantify
the effect of other mutations in other viral genes
involved in HIV-1 replication, including, but not limited
25 to the gag, pol, and envelope genes.

30 Fitness test vectors engineered by site directed
mutagenesis to contain specific mutations in integrase
were tested in a fitness assay to determine accurately and
quantitatively the relative fitness compared to a well-
characterized reference standard.

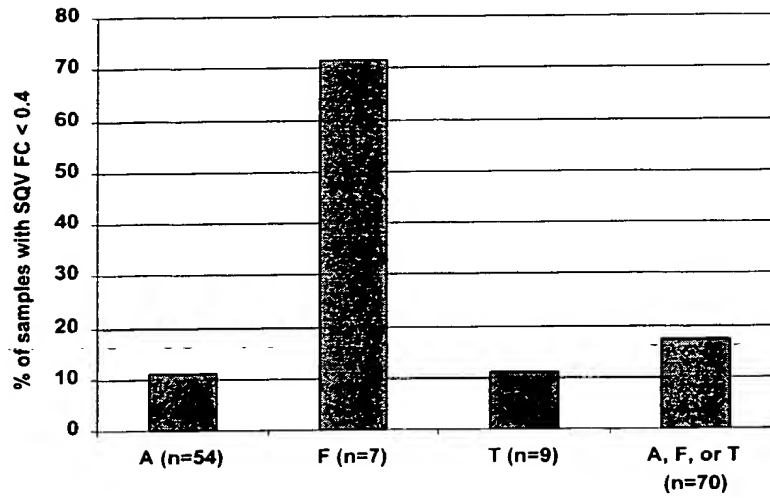
Genotypic changes that are observed to correlate with
resistance to integrase inhibitors are evaluated by

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5 construction of fitness vectors containing the specific
mutation on a defined, wild-type (drug susceptible)
genetic background. Mutations may be incorporated alone
and/or in combination with other mutations that are
10 thought to modulate the fitness of a virus. Mutations
are introduced into the fitness test vector through any of
the widely known methods for site-directed mutagenesis. In
one embodiment of this invention the mega-primer PCR
method for site-directed mutagenesis is used (Sarkar, G.
and Sommer, S.S., 1994, Biotechniques 8, 404-407). A
15 fitness test vector containing the specific mutation or
group of mutations are then tested using the fitness assay
described in Example 10 and the fitness is compared to
that of a genetically defined wild-type (drug susceptible)
fitness test vector which lacks the specific mutations.
20 Observed changes in fitness are attributed to the specific
mutations introduced into the fitness test vector. In
several related embodiments of the invention, fitness test
vectors containing site directed mutations in integrase
that result in amino acid substitutions at positions 66,
25 154, 66 and 153, and 66 and 154 are constructed and tested
for fitness (Figure 7). As controls, mutants with
multiple changes conferring resistance to reverse
transcriptase and protease inhibitors (MDRC4) and with a
mutation in the integrase active site (D64V) were also
30 tested. The fitness results enable the correlation
between specific integrase amino acid substitutions and
changes in viral fitness.

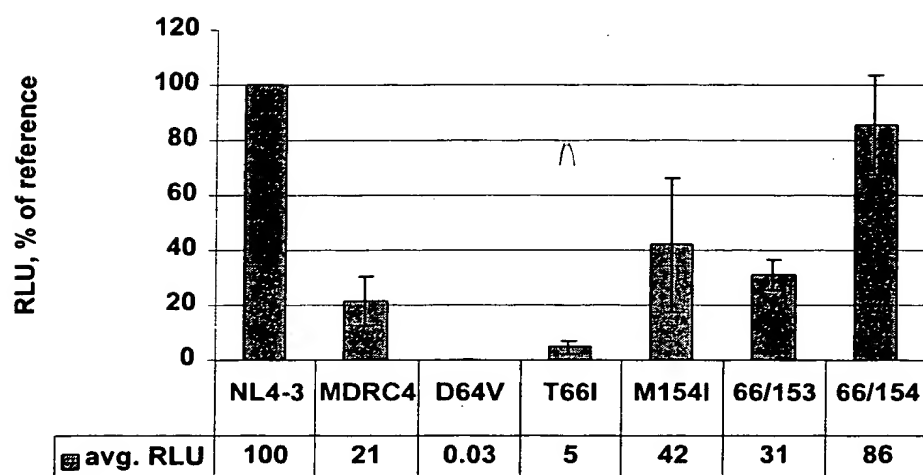
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- 5 Figure 6. Distribution of saquinavir hyper-susceptibility by amino acid change at position 82.



5

Figure 7. Relative luciferase activity of integrase inhibitor-resistant site-directed mutants.



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Table 1: PRI susceptibility of selected patient samples. Viruses displaying increased susceptibility to amprenavir (5-fold or greater) were genotyped and found to contain the N88S mutation in PR. Samples were listed in order of decreasing amprenavir susceptibility.

Table 1

Sample ID	Experience	Fold Change vs. Reference					PR Mutations
		Prior PRI	SQV	IDV	RTV	NFV AMP	
0732	NFV	0.73	2.11	1.72	6.92	0.08	K14R, I15V, K20T, E35D, M36I, R41K, I62V, L63Q, N88S
627	IDV	0.26	6.16	1.50	21.06	0.09	I131V, E35D, M46L, L63P, I64V, I73V, N88S
1208	NFV	1.55	3.15	1.22	11.06	0.10	I62V, L63P, V77I, N88S
360	IDV	1.88	6.31	1.49	29.95	0.15	I13V, K20M, M36V, N37A, M46I, I62V, L63P, N88S, I93L
0910	NFV	1.41	5.47	1.85	16.76	0.16	M46I, L63P, V77I, N88S, I93I/L
3542	IDV	1.28	7.61	3.36	24.67	0.16	I13V, K14R, N37D, M46I, L63P, N88S, I93L
3654		1.80	7.56	1.95	18.61	0.20	I13V, R41K, M46I, L63P, V77I, N88S, I93L

Fold Change Limits: >2.5 <0.4

- 5 Table 2: PRI susceptibility of site-directed mutants in PR. Mutations were introduced into the drug sensitive reference resistance test vector and the susceptibility to PRIs was determined.

Table 2

Site-Directed Mutations	Fold Change vs. reference				
	SQV	IDV	RTV	NFV	AMP
L63P	1.04	1.12	1.27	1.43	1.06
L63P, V77I	1.24	1.72	1.73	2.49	0.91
N88S	0.47	1.56	0.36	2.39	0.04
L63P, N88S	1.44	2.56	0.77	5.10	0.11
L63P, V77I, N88S	1.24	3.09	1.39	12.69	0.08
M46L, L63P, N88S	1.15	2.30	0.85	8.18	0.12
M46L, L63P, V77I, N88S	1.45	2.97	1.33	12.24	0.14

FOLD CHANGE LIMITS: <0.4 >2.5

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5 Table 3: Relative luciferase activity levels for patient
sample virus-derived resistance test vector pools. The
luciferase activity (relative light units, RLU) measured
10 in the absence of drug for the patient sample was compared
to that of the drug sensitive reference control from the
same assay run, and expressed as a percentage of control.
These values are from one assay each. All the samples
that contain the N88S mutations in PR were found to have
15 reduced luciferase activity compared to control.

Table 3

Sample ID PR Mutations		Relative Luciferase Activity (% of control)
0732	K14R, I15V, K20T, E35D, M36I, R41K, I62V, L63Q, N88S	8.5
627	I131V, E35D, M46L, L63P, I64V, I73V, N88S	0.7
1208	I62V, L63P, V77I, N88S	14.2
360	I13V, K20M, M36V, N37A, M46I, I62V, L63P, N88S, I93L	2.2
0910	M46I, L63P, V77I, N88S, I93I/L	16.0
3542	I13V, K14R, N37D, M46I, L63P, N88S, I93L	4.6
3654	I13V, R41K, M46I, L63P, V77I, N88S, I93L	12.8

5 Table 4: Relative luciferase activity levels for
resistance test vectors containing site-directed
mutations. The luciferase activity (relative light units,
RLU) measured in the absence of drug for the mutant was
10 compared to that of the drug sensitive reference control
from the same assay run, and expressed as a percentage of
control. These values are from one to five assays each,
and each value was obtained using an independent clone for
15 mutants which were tested multiple times. All the
constructs that contain the N88S mutations in PR were
found to have reduced luciferase activity compared to
control. All the constructs with the K20T mutation were
essentially inactive in the assay.

Table 4

Site-Directed Mutations	Average Luciferase Activity	
	(% of control)	number of clones tested
L63P	163.9	1
L63P, V77I	75.6	1
N88S	1.0	3
L63P, N88S	20.7	2
L63P, V77I, N88S	29.3	2
M46L, L63P, N88S	28.0	2
M46L, L63P, V77I, N88S	53.2	5
K20T, N88S	<0.01	5
K20T, L63P, N88S	<0.01	1

5 Table 5: Oligonucleotide primers used for PCR amplification and for generating site-directed mutants.

Sub aa!

Table 5.

Primer name:			
#1: PCR6	5'	CCAATTRYTGATATTCTCATGNTCHICTTGGG	3' (35-mer)
#2: PDS/Apa	5'	CATGTTGCAGGGCCCCCTAGGAAAAAGGGCTGTTGGAAATGTG	3' (42-mer)
#3: PDS/Age	5'	CACTCCATGTACCGGTTCTTTAGAATTCYCTG	3' (34-mer)
#4: RsrII	5'	ACTTTCGGACCGTCCATTCTGGCTTAATTTTACTGGTACAG	3' (43-mer)
#5: K20T	5'	GGGGGGCAATTAACGGAAGCTCTATTAG	3' (28-mer)
#6: M46L	5'	GATGGAAACCAAAATTGATAGCGGGAATTG	3' (30-mer)
#7: L63P	5'	GTATGATCAGATACCCATAGAAATCTGC	3' (28-mer)
#8: N88S	5'	CTGAGTCAACAGACTTCTTCAATTATG	3' (28-mer)

R = A or G
Y = C or T
N = A, C, G, or T
H = A, C, or T

35 Table 6. PRI Susceptibility (Fold Change <2.5) of Viruses with Mutations at 82 and/or 90

Percent of viruses with indicated primary mutation(s) which are drug sensitive (fold change in IC50 < 2.5)

drug	V82A/F/S/T	L90M	V82A/F/S/T and L90M
RTV	8.0	27.6	3.0
NFV	20.0	8.6	3.0
IDV	22.7	31.0	9.1
AMP	53.3	65.5	33.3
SQV	73.3	46.6	21.2

5

Table 7. Correlation Between 82A/F/S/T, Secondary Mutations, and IDV Susceptibility.

	position	n	% FC > 2.5	chi square p
10	24	20	100%	<0.005
	71	27	100%	<0.0001
	54	38	95%	<0.0001
	46	35	89%	<0.01
15	10	47	83%	<0.05
	63	72	79%	<0.05
	82	75	77%	

20 all virus with V82A/F/S/T and no other primary mutations.

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5 **Table 8. Correlation Between 82A/F/S/T, Secondary Mutations, and SQV Susceptibility.**

position	n	% FC > 2.5	chi square p
20	5	80%	<0.001
36	11	73%	<0.001
24	20	65%	<0.0001
71	27	52%	<0.0001
54	38	47%	<0.0001
10	47	40%	<0.001
82	75	27%	

all virus

20 **Table 9. Association Between SQV and IDV Susceptibility, V82A/F/S/T, and Number of Resistance Associated Mutations**

Number of secondary mutations	Number of samples	% with IDV FC > 2.5	% with SQV FC > 2.5
1	75	77	27
2	67	82	30
3	51	88	39
4	38	95	50
5	25	96	60
6	17	100	76
7	5	100	60

5

Table 10. Correlation Between L90M, Secondary Mutations, and IDV Susceptibility.

position	n	% FC > 2.5	chi square p
73	19	89%	<0.01
71	18	89%	<0.001
46	25	88%	<0.05
90	58	69%	

15

all viruses with L90M and

Table 11. Correlation Between L90M, Secondary Mutations, and SQV Susceptibility.

position	n	% FC > 2.5	chi square p
73	19	79%	<0.01
71	18	78%	<0.001
77	25	76%	<0.05
10	34	65%	<0.05
90	58	55%	

25

all viruses

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Table 12. Association Between SQV and IDV Susceptibility, L90M, and Number of Resistance Associated Mutations.

	Number of secondary mutations	Number of samples	% w with IDV FC > 2.5	% w with SQV FC > 2.5
	0	58	69	53
	1	57	70	47
	2	56	70	48
	3	41	80	68
	4	31	87	77
	5	14	100	100
	6	6	100	100

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Summary of the Invention

In another embodiment of this invention, a method is provided of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

- (a) collecting a biological sample from the HIV-infected patient;
- (b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 84, 48, 23, 73, 53, 33, 74, 20, 90, 32 and 39 or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 66, 84, 54, 48, 33, 73, 20, 71, 64 and 93, and
- (c) determining a change in susceptibility to a protease inhibitor, wherein the protease inhibitor is saquinavir.

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 84, 48, 23, 73, 53, 33, 74, 20, and 90, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 66, 84, 54, 48, 33, 73, 20, and 71, wherein the change in susceptibility in step (c) is a decrease in susceptibility to saquinavir.

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and

a secondary mutation at codons 32 or 39, or a mutation at codon 90 and a secondary mutation at codons 64 or 93, wherein the change in susceptibility in step (c) is an increase in susceptibility to saquinavir.

5

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 95, 54, 84, 82, 46, 13, and 74, wherein the protease inhibitor is indinavir.

10

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 95, 54, 84, 82, and 46, wherein the change in susceptibility in step (c) is a decrease in susceptibility to indinavir.

15

20

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 90 and a secondary mutation at codons 13 or 74, wherein the change in susceptibility in step (c) is an increase in susceptibility to indinavir.

25

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, 90, 13, 48, 23, 84, 53, 74, 60, 33, 36, 35, 32, and 46 or a mutation at codon

30

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90 and a secondary mutation at codons selected from the group consisting of 95, 55, 54, 82, 85, 84, 20, 72, 62, 74, 53, 48, 23, 58, 36, 64, 77, and 93.

5 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, wherein the protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir.

10 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, wherein step (c) is determining a change in susceptibility to the protease inhibitor greater than 10 fold.

15 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 48, 23, 84, 53, 74, 20, 60, 33, 36, 35, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 84, 53, 48, 23, 58, 20, 36, and 54, wherein the change in susceptibility in step (c) is a decrease in susceptibility to saquinavir.

20 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and a secondary mutation at codons 32 or 46, or a mutation at codon 90 and a secondary mutation at codons 64, 77, or 93, wherein the change in susceptibility in step (c) is an increase in susceptibility to saquinavir.

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5 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, and 90, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 95, 55, 54, 82, 85, 84, 20, 72, and 62, wherein the change in susceptibility in step (c) is a decrease in susceptibility to indinavir.

10 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and a secondary mutation at codon 13, or a mutation at codon 15 90 and a secondary mutation at codon 74, wherein the change in susceptibility in step (c) is an increase in susceptibility to indinavir.

20 In another embodiment of this invention, a method is provided of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

- 25 (a) collecting a biological sample from the HIV-infected patient;
- (b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and secondary mutations of at least three codons; and
- 30 (c) determining a decrease in susceptibility to saquinavir.

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease

antiretroviral therapy, wherein in the evaluating step (b), the nucleic acid encoding HIV protease has secondary mutations of at least five codons.

5 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, wherein the secondary mutation are selected from the group consisting of codons 10, 20, 52, 53, 54, 66, 71, 73 and 84.

10 In another embodiment of this invention, a method is provided of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

- 15 (a) collecting a biological sample from the HIV-infected patient;
- (b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and secondary mutations at codons selected from the group consisting of 33, 23, 84, 32, 53, 90, 37, 71, 46, 10, 54, 61, 11, and 46, or a mutation at codon 90 and secondary mutations at codons selected from the group consisting of 89, 53, 84, 33, 92, 95, 54, 58, 46, 82, 36, 10, 62, 74, 15, 47, 66, 32, 55, 53, 13, and 69; and
- 25 (c) determining a change in susceptibility to amprenavir.

30 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, wherein the mutation at codon 82 is a substitution of alanine (A), phenylalanine (F),

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serine (S), or threonine (T) for valine(V) and the mutation at codon 90 is a substitution of methionine (M) for leucine (L).

5 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and secondary mutations at codons selected from the group consisting of 33, 23, 84, 32, 53, 90, 37, 71, 46, 10, 54, 10 11, and 46, or a mutation at codon 90 and secondary mutations at codons selected from the group consisting of 89, 53, 84, 33, 92, 95, 54, 58, 46, 82, 36, 10, 62, 47, 66, 32, 55, 53, and 13; wherein the change in susceptibility in step (c) is a decrease in susceptibility 15 to saquinavir.

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and 20 a secondary mutation at codon 61, or a mutation at codon 90 and secondary mutations at codons 74, 15, or 69, wherein the change in susceptibility in step (c) is an increase in susceptibility to saquinavir.

25 In another embodiment of this invention, a resistance test vector is provided comprising an HIV patient-derived segment comprising nucleic acid encoding protease having a mutation at codon 82 and secondary mutations at codons selected from the group consisting of 73, 55, 48, 20, 43, 30 53, 90, 13, 84, 23, 33, 74, 32, 39, 60, 36, and 35, or a mutation at codon 90 and secondary mutations at codons selected from the group consisting of 53, 95, 54, 84, 82, 46, 13, 74, 55, 85, 20, 72, 62, 66, 84, 48, 33, 73, 71,

64, 93, 23, 58, and 36 and an indicator gene, wherein the expression of the indicator gene is dependent upon the patient-derived segment.

5 In another embodiment of this invention, the above resistance test vector is provided, wherein the mutation of the patient derived segment at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine(V) and the mutation at
10 codon 90 is a substitution of methionine (M) for leucine (L).

Phenotypic Susceptibility:

Phenotypic assays provide information relating to drug
15 resistance in the form of a fold-change in IC50 value, i.e. the ratio of the IC50 for the patient virus to that of a drug sensitive reference control. The significance of the fold change value with respect to treatment choices is limited by at least two factors: the reproducibility of
20 the assay, and the achievable drug concentration at the site of action in the patient. For the PhenoSense™ assay described herein, the reproducibility cut-off is 2.5-fold. For most protease inhibitors, the level of reduction in susceptibility required to overcome the achievable plasma
25 drug concentration is not well defined. However retrospective clinical studies using the 2.5-fold cutoff have suggested that this value is useful for predicting response to protease inhibitors, at least when used alone or in combination with reverse transcriptase inhibitors.
30 Recently, the use of dual protease inhibitor based regimens (typically involving co-dosing of an inhibitor with ritonavir or nelfinavir) has become popular, since the plasma drug levels can be significantly boosted due to

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inhibition of metabolic pathways. In cases such as these, it is likely that the clinically relevant fold-change cutoff will be higher, perhaps 10-fold. Future clinical studies will be required in order to accurately determine the actual clinical cutoff value.

As used herein, what it is understood to mean "secondary mutations" in addition to the discussion on pages 7 and 8 of this specification, is that other mutations, not currently recognized as resistance-associated, may also be defined as "secondary mutations" if they enhance the effects of primary mutations.

Example 17

Predicting Response to Protease Inhibitors by Characterization of Amino Acid 82 of HIV-1 Protease.

In one embodiment of this invention, changes in the amino acid at position 82 of the protease protein of HIV-1 are evaluated using the following method comprising: (i) collecting a biological sample from an HIV-1 infected subject; (ii) evaluating whether the biological sample contains nucleic acid encoding HIV-1 protease having a valine to alanine (V82A), phenylalanine (V82F), serine (V82S), threonine (V82T), or other amino acid substitution at codon 82 ("V82 mutations"); and (iii) determining susceptibility to protease inhibitors (PRI).

The biological sample comprises whole blood, blood components including peripheral mononuclear cells (PBMC), serum, plasma (prepared using various anticoagulants such as EDTA, acid citrate-dextrose, heparin), tissue biopsies, cerebral spinal fluid (CSF), or other cell, tissue or body

fluids. In another embodiment, the HIV-1 nucleic acid (genomic RNA) or reverse transcriptase protein can be isolated directly from the biological sample or after purification of virus particles from the biological sample. Evaluating whether the amino acid at position 82 of the HIV-1 protease is mutated to alanine, phenylalanine, serine, threonine, or other amino acids, can be performed using various methods, such as direct characterization of the viral nucleic acid encoding protease or direct characterization of the protease protein itself. Defining the amino acid at position 82 of protease can be performed by direct characterization of the protease protein by conventional or novel amino acid sequencing methodologies, epitope recognition by antibodies or other specific binding proteins or compounds. Alternatively, the amino acid at position 82 of the HIV-1 protease protein can be defined by characterizing amplified copies of HIV-1 nucleic acid encoding the protease protein. Amplification of the HIV-1 nucleic acid can be performed using a variety of methodologies including reverse transcription-polymerase chain reaction (RT-PCR), NASBA, SDA, RCR, or 3SR. The nucleic acid sequence encoding HIV protease at codon 82 can be determined by direct nucleic acid sequencing using various primer extension-chain termination (Sanger, ABI/PE and Visible Genetics) or chain cleavage (Maxam and Gilbert) methodologies or more recently developed sequencing methods such as matrix assisted laser desorption-ionization time of flight (MALDI-TOF) or mass spectrometry (Sequenom, Gene Trace Systems). Alternatively, the nucleic acid sequence encoding amino acid position 82 can be evaluated using a variety of probe hybridization methodologies, such as genechip

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hybridization sequencing (Affymetrix), line probe assay (LiPA; Murex), and differential hybridization (Chiron).

5 In a preferred embodiment of this invention, evaluation of
protease inhibitor susceptibility and of whether amino
acid position 82 of HIV-1 protease was wild type or mutant
was carried out using a phenotypic susceptibility assay or
genotypic assay, respectively, using resistance test
vector DNA prepared from the biological sample. In one
10 embodiment, plasma sample was collected, viral RNA was
purified and an RT-PCR methodology was used to amplify a
patient derived segment encoding the HIV-1 protease and
reverse transcriptase regions. The amplified patient
derived segments were then incorporated, via DNA ligation
15 and bacterial transformation, into an indicator gene viral
vector thereby generating a resistance test vector.
Resistance test vector DNA was isolated from the bacterial
culture and the phenotypic susceptibility assay was
carried out and analyzed as described in Example 1.

20 The nucleic acid (DNA) sequence of the patient derived
HIV-1 protease and reverse transcriptase regions was
determined using a fluorescence detection chain
termination cycle sequencing methodology (ABI/PE). The
25 method was used to determine a consensus nucleic acid
sequence representing the combination of sequences of the
mixture of HIV-1 variants existing in the subject sample
(representing the quasispecies), and to determine the
nucleic acid sequences of individual variants. Genotypes
30 are analyzed as lists of amino acid differences between
virus in the patient sample and a reference laboratory
strain of HIV-1, NL4-3. Genotypes and corresponding
phenotypes (fold-change in IC50 values) are entered in a

relational database linking these two results with patient information. Large datasets can then be assembled from patient virus samples sharing particular characteristics, such as the presence of any given mutation or reduced susceptibility to any drug or combination of drugs.

(a) Protease inhibitor susceptibility of viruses containing mutations at amino acid 82 of HIV-1 Protease.

Phenotypic susceptibility profiles of 270 patient virus samples that contained a mutation at position 82 (but not at positions 30 or 50, which are primary mutations associated with resistance to nelfinavir and amprenavir, respectively) were analyzed. According to most published guidelines, such viruses are expected to be resistant to ritonavir, nelfinavir, indinavir, and saquinavir. However, only 61.7% of these samples displayed reduced susceptibility to saquinavir using a 2.5-fold threshold (Table 13), while 31.2% and 40.0% displayed reduced susceptibility to saquinavir and indinavir, respectively, using a 10-fold threshold (Table 14). Thus, there was poor correlation between the presence of mutations at position 82 and saquinavir or indinavir susceptibility.

(b) Indinavir susceptibility (fold change threshold 10) of viruses containing combinations of mutations at amino acid 82 and one secondary mutation in HIV-1 Protease.

To explore the possibility that indinavir resistance (fold change in IC50 > 10-fold) in viruses containing mutations at position 82 requires the presence of other specific mutations, decreased indinavir susceptibility (fold-change in IC50 greater than 10) in viruses containing V82

mutations was correlated with the presence of mutations at other positions. This analysis revealed several positions (most strongly 73, 55, 48, 20, 43, 53, and 90) that decreased indinavir susceptibility significantly in combination with V82 mutations, compared to when these other mutations were absent (see Table 15). The presence of a mutation at position 13 significantly decreased the proportion of samples that had reduced indinavir susceptibility (45.9% vs. 62.2%; Table 15). In other words, the absence of a mutation at position 13 was correlated with decreased susceptibility to indinavir.

(c) Saquinavir susceptibility (fold change threshold-2.5) of viruses containing combinations of mutations at amino acid 82 and one secondary mutation in HIV-1 Protease.

To explore the possibility that saquinavir resistance in viruses containing mutations at position 82 requires the presence of other specific mutations, decreased saquinavir susceptibility (fold-change in IC50 greater than 2.5-fold) in viruses containing V82 mutations was correlated with the presence of mutations at other positions. This analysis revealed that several positions (most strongly 84, 48, 23, 73, 53, 33, 74, 20, and 90) were associated with reduced saquinavir susceptibility (See Table 16). The combination of mutations at position 82 with a mutation at position 32 or 39 significantly decreased the proportion of samples that had reduced saquinavir susceptibility (Table 16). In other words, the absence of a mutation at position 32 or 39 was correlated with decreased susceptibility to indinavir.

(d) Saquinavir susceptibility (fold change threshold 10) of viruses containing combinations of mutations at amino acid 82 and one secondary mutation in HIV-1 Protease.

5 To explore the possibility that saquinavir resistance in
viruses containing mutations at position 82 requires the
presence of other specific mutations, decreased saquinavir
susceptibility (fold-change in IC50 greater than 10 fold)
10 in viruses containing V82 mutations was correlated with
the presence of mutations at other positions. This
analysis revealed that several positions (most strongly
48, 23, 84, 53, 74, 20, 60, 33, 36, 35, and 90) were
associated with reduced saquinavir susceptibility (See
Table 17). The combination of mutations at position 82
15 with a mutation at position 32 or 46 significantly
decreased the proportion of samples that had reduced
saquinavir susceptibility (Table 17). In other words, the
absence of a mutation at position 32 or 46 was correlated
with decreased susceptibility to indinavir.

Example 18

**Predicting Response to Protease Inhibitors by
Characterization of Amino Acid 90 of HIV-1 Protease.**

25 In one embodiment of this invention, changes in the amino
acid at position 90 of the protease protein of HIV-1 are
evaluated using the following method comprising: (i)
collecting a biological sample from an HIV-1 infected
subject; (ii) evaluating whether the biological sample
30 contains nucleic acid encoding HIV-1 protease having a
leucine to methionine (L90M) substitution at codon 90; and
(iii) determining susceptibility to protease inhibitors
(PRI).

The biological sample comprises whole blood, blood components including peripheral mononuclear cells (PBMC), serum, plasma (prepared using various anticoagulants such as EDTA, acid citrate-dextrose, heparin), tissue biopsies, cerebral spinal fluid (CSF), or other cell, tissue or body fluids. In another embodiment, the HIV-1 nucleic acid (genomic RNA) or reverse transcriptase protein can be isolated directly from the biological sample or after purification of virus particles from the biological sample. Evaluating whether the amino acid at position 90 of the HIV-1 protease is mutated to methionine, can be performed using various methods, such as direct characterization of the viral nucleic acid encoding protease or direct characterization of the protease protein itself. Defining the amino acid at position 90 of protease can be performed by direct characterization of the protease protein by conventional or novel amino acid sequencing methodologies, epitope recognition by antibodies or other specific binding proteins or compounds. Alternatively, the amino acid at position 90 of the HIV-1 protease protein can be defined by characterizing amplified copies of HIV-1 nucleic acid encoding the protease protein. Amplification of the HIV-1 nucleic acid can be performed using a variety of methodologies including reverse transcription-polymerase chain reaction (RT-PCR), NASBA, SDA, RCR, or 3SR. The nucleic acid sequence encoding HIV protease at codon 90 can be determined by direct nucleic acid sequencing using various primer extension-chain termination (Sanger, ABI/PE and Visible Genetics) or chain cleavage (Maxam and Gilbert) methodologies or more recently developed sequencing methods such as matrix assisted laser desorption-ionization time of flight (MALDI-TOF) or mass

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spectrometry (Sequenom, Gene Trace Systems). Alternatively, the nucleic acid sequence encoding amino acid position 90 can be evaluated using a variety of probe hybridization methodologies, such as genechip hybridization sequencing (Affymetrix), line probe assay (LiPA; Murex), and differential hybridization (Chiron).

In a preferred embodiment of this invention, evaluation of protease inhibitor susceptibility and of whether amino acid position 90 of HIV-1 protease was wild type or methionine, was carried out using a phenotypic susceptibility assay or genotypic assay, respectively, using resistance test vector DNA prepared from the biological sample. In one embodiment, plasma sample was collected, viral RNA was purified and an RT-PCR methodology was used to amplify a patient derived segment encoding the HIV-1 protease and reverse transcriptase regions. The amplified patient derived segments were then incorporated, via DNA ligation and bacterial transformation, into an indicator gene viral vector thereby generating a resistance test vector. Resistance test vector DNA was isolated from the bacterial culture and the phenotypic susceptibility assay was carried out and analyzed as described in Example 1. The nucleic acid (DNA) sequence of the patient derived HIV-1 protease and reverse transcriptase regions was determined using a fluorescence detection chain termination cycle sequencing methodology (ABI/PE). The method was used to determine a consensus nucleic acid sequence representing the combination of sequences of the mixture of HIV-1 variants existing in the subject sample (representing the quasispecies), and to determine the nucleic acid sequences of individual variants. Genotypes are analyzed as lists of

amino acid differences between virus in the patient sample and a reference laboratory strain of HIV-1, NL4-3. Genotypes and corresponding phenotypes (fold-change in IC50 values) are entered in a relational database linking these two results with patient information. Large datasets can then be assembled from patient virus samples sharing particular characteristics, such as the presence of any given mutation or reduced susceptibility to any drug or combination of drugs.

(a) Protease inhibitor susceptibility of viruses containing mutations at amino acid 90 of HIV-1 Protease.

Phenotypic susceptibility profiles of 333 patient virus samples which contained a mutation at position 90 (L90M) but not at positions 30 or 50, which are primary mutations associated with resistance to nelfinavir and amprenavir, respectively) were analyzed. According to most published guidelines, such viruses are expected to be resistant to ritonavir, nelfinavir, indinavir, and saquinavir. However, only 79.3% and 84.7% of these samples displayed reduced susceptibility to saquinavir and indinavir, respectively, using a 2.5-fold threshold (Table 13), while 43.5% and 53.8% displayed reduced susceptibility to saquinavir and indinavir, respectively, using a 10-fold threshold (Table 14). Thus, there was poor correlation between the presence of mutations at position 90 and saquinavir or indinavir susceptibility.

(b) Indinavir susceptibility (fold change threshold 2.5) of viruses containing combinations of mutations at amino acid 90 and one secondary mutation in HIV-1 Protease.

5 To explore the possibility that indinavir resistance in
viruses containing a mutation at position 90 requires the
presence of other specific mutations, decreased indinavir
susceptibility (fold-change in IC50 greater than 2.5) in
10 viruses containing L90M was correlated with the presence
of mutations at other positions. This analysis revealed
several other positions (most strongly 53, 95, 54, 84, 82
and 46) that decreased indinavir susceptibility
significantly in combination with the L90M mutation,
15 compared to when these other mutations were absent (see
Table 18). The presence of a mutation at position 13 or 74
significantly decreased the proportion of samples that had
reduced indinavir susceptibility (Table 18). In other
words, the absence of mutations at position 13 or 74 was
correlated with decreased susceptibility to indinavir.

20 **(c) Indinavir susceptibility (fold change threshold 10) of
viruses containing combinations of mutations at amino acid
90 and one secondary mutation in HIV-1 Protease.**

25 To explore the possibility that indinavir resistance in
viruses containing a mutation at position 90 requires the
presence of other specific mutations, decreased indinavir
susceptibility (fold-change in IC50 greater than 10) in
viruses containing L90M was correlated with the presence
30 of mutations at other positions. This analysis revealed
several secondary positions (most strongly 95, 55, 54, 82,
85, 84, 20, 72, and 62) that decreased indinavir
susceptibility significantly in combination with the L90M

mutation, compared to when these other mutations were absent (see Table 19). The presence of a mutation at position 74 significantly decreased the proportion of samples that had reduced indinavir susceptibility (27.5% vs. 57.3%; Table 19). In other words, the absence of a mutation at position 74 was correlated with decreased susceptibility to indinavir.

(d) Saquinavir susceptibility (fold change threshold 2.5) of viruses containing combinations of mutations at amino acid 90 and one secondary mutation in HIV-1 Protease.

To explore the possibility that saquinavir resistance in viruses containing a mutation at position 90 requires the presence of other specific mutations, decreased saquinavir susceptibility (fold-change in IC50 greater than 2.5) in viruses containing L90M was correlated with the presence of mutations at other positions. This analysis revealed several other positions (most strongly 53, 66, 84, 54, 48, 33, 73, 20, and 71) that decreased saquinavir susceptibility significantly in combination with the L90M mutation, compared to when these other mutations were absent (see Table 20). The presence of a mutation at position 64 or 93 significantly decreased the proportion of samples that had reduced saquinavir susceptibility (Table 20). In other words, the absence of a mutation at position 64 or 93 was correlated with decreased susceptibility to saquinavir.

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(e) Saquinavir susceptibility (fold change threshold 10) of viruses containing combinations of mutations at amino acid 90 and one secondary mutation in HIV-1 Protease.

5 To explore the possibility that saquinavir resistance in
viruses containing a mutation at position 90 requires the
presence of other specific mutations, decreased saquinavir
susceptibility (fold-change in IC50 greater than 10) in
10 viruses containing L90M was correlated with the presence
of mutations at other positions. This analysis revealed
several other positions (most strongly 84, 53, 48, 23, 58,
20, 36, and 54) that decreased saquinavir susceptibility
significantly in combination with the L90M mutation,
15 compared to when these other mutations were absent (see
Table 21). The presence of a mutation at position 64, 77
or 93 significantly decreased the proportion of samples
that had reduced saquinavir susceptibility (Table 21). In
other words, the absence of a mutation at position 64, 77
or 93 was correlated with decreased susceptibility to
20 saquinavir.

(f) Saquinavir susceptibility (fold change threshold 2.5) of viruses containing combinations of mutations at amino acid 90 and many secondary mutations in HIV-1 Protease.

25 To explore the possibility that saquinavir resistance in
viruses containing mutations at position 90 requires the
presence of some defined number of other mutations,
decreased saquinavir susceptibility (fold-change in IC50
30 greater than 2.5) in viruses containing L90M was
correlated with the number of mutations at secondary
positions. The following positions were considered: 10,
20, 52, 53, 54, 66, 71, 73, and 84; positions 53 and 84

were weighted twice, yielding a saquinavir resistance-associated mutation count. This analysis revealed that 100% of samples with L90M and a mutation count of at least 5 had reduced saquinavir susceptibility (See Table 22). Combination with 3 or 4 other secondary mutations also significantly increased the proportion of samples that had reduced saquinavir susceptibility (85.7% and 97.3%, respectively; see Table 22).

Table 13. PRI Susceptibility of Viruses with Mutations at 82 and/or 90 (fold change threshold > 2.5).

Drug	Percent of viruses with indicated primary mutation(s) with reduced susceptibility (fold change in IC ₅₀ > 2.5)	
	V82 mutations	L90M
Amprenavir	60.0	60.4
Indinavir	92.2	84.7
Nelfinavir	94.4	97.0
Ritonavir	97.8	93.4
Saquinavir	61.7	79.3

Table 14. PRI Susceptibility of Viruses with Mutations at 82 and/or 90 (fold change threshold > 10).

Drug	Percent of viruses with indicated primary mutation(s) with reduced susceptibility (fold change in IC ₅₀ > 10)	
	V82 mutations	L90M
Amprenavir	10.4	12.9
Indinavir	60.0	53.8
Nelfinavir	68.9	74.5
Ritonavir	89.3	66.1
Saquinavir	31.2	43.5

Table 15. Correlation Between V82 mutations, Secondary Mutations, and Indinavir Susceptibility (fold change threshold > 10).

	position	+	or -	n	mt % >10	wt %>10	p value
5	73	+		22	90.9	57.3	0.0011
	55	+		25	80.0	58.0	0.0238
	48	+		35	77.1	57.4	0.0188
	20	+		77	76.6	53.4	<0.001
10	43	+		34	76.5	57.6	0.0258
	53	+		33	75.8	57.8	0.0349
	90	+		135	74.1	45.9	<0.001
	72	+		56	73.2	56.5	0.0160
	35	+		91	72.5	53.6	0.0019
15	54	+		188	71.3	34.1	<0.001
	71	+		184	70.7	37.2	<0.001
	36	+		99	69.7	54.4	0.0091
	10	+		224	66.1	30.4	<0.001
	82			270	60.0		
20	13	-		37	45.9	62.2	0.0458

Table 16. Correlation Between V82 mutations, Secondary Mutations, and Saquinavir Susceptibility (fold change threshold > 2.5)

	position	+	or -	n	mt % >2.5	wt %>2.5	p value
25	84	+		36	100.0	55.8	<0.001
	48	+		35	97.1	56.4	<0.001
	23	+		11	90.9	60.5	0.0358
30	73	+		22	90.9	59.1	0.0018
	53	+		33	87.9	58.1	<0.001
	33	+		24	87.5	59.2	0.0041
	74	+		25	84.0	59.4	0.0113
	20	+		77	83.1	53.1	<0.001
35	90	+		135	82.2	41.0	<0.001
	43	+		34	79.4	59.1	0.0162
	36	+		99	75.8	53.5	<0.001
	41	+		79	74.7	56.3	0.0032
	54	+		187	74.3	32.9	<0.001
40	71	+		183	74.3	34.9	<0.001
	35	+		91	73.6	55.6	0.0028
	10	+		223	69.5	23.9	<0.001
	82			269	61.7		
	32	-		24	37.5	64.1	0.0106
45	39	-		4	0.0	62.6	0.0207

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Table 17. Correlation Between V82 mutations, Secondary Mutations, and Saquinavir Susceptibility (fold change threshold > 10)

	position	+ or -	n	mt % >10	wt %>10	p value
5	48	+	35	82.9	23.5	<0.001
	23	+	11	81.8	29.1	<0.001
	84	+	36	72.2	24.9	<0.001
	53	+	33	69.7	25.8	<0.001
10	74	+	25	56.0	28.7	0.0062
	20	+	77	55.8	21.4	<0.001
	60	+	30	50.0	28.9	0.0181
	33	+	24	50.0	29.4	0.0352
	36	+	99	47.5	21.8	<0.001
15	35	+	91	44.0	24.7	0.0011
	90	+	135	43.0	19.4	<0.001
	41	+	79	41.8	26.8	0.0126
	62	+	119	41.2	23.3	0.0013
	54	+	187	39.0	13.4	<0.001
20	71	+	183	37.7	17.4	<0.001
	10	+	223	35.0	13.0	0.0019
	82		269	31.2		
	46	-	156	26.3	38.1	0.0275
	32	-	24	12.5	33.1	0.0268

Table 18. Correlation Between L90M, Secondary Mutations, and Indinavir Susceptibility (fold change threshold > 2.5).

	position	+ or -	n	mt % >2.5	wt %>2.5	p value
	53	+	29	100.0	83.2	0.0064
	95	+	23	100.0	83.5	0.0189
	54	+	129	98.4	76.0	<0.001
35	84	+	104	97.1	79.0	<0.001
	82	+	135	94.1	78.3	<0.001
	46	+	164	93.3	76.3	<0.001
	73	+	117	92.3	80.6	0.0027
	71	+	233	91.4	69.0	<0.001
40	20	+	115	91.3	81.2	0.0095
	10	+	255	90.2	66.7	<0.001
	63	+	325	85.5	50.0	0.0214
	90		333	84.7		
	13	-	77	76.6	87.1	0.0226
45	74	-	40	67.5	87.0	0.0028

Table 19. Correlation Between L90M, Secondary Mutations, and Indinavir Susceptibility (fold change threshold > 10).

	position	+	or -	n	mt % >10	wt % >10	p value
5	95	+		23	82.6	51.6	0.0030
	55	+		22	81.8	51.8	0.0048
	54	+		129	81.4	36.3	<0.001
	82	+		135	74.1	39.9	<0.001
	85	+		23	73.9	52.3	0.0346
10	84	+		104	70.2	46.3	<0.001
	20	+		115	66.1	47.2	0.0103
	72	+		87	64.4	50.0	0.0141
	62	+		154	63.6	45.3	<0.001
	46	+		164	63.4	44.4	<0.001
15	36	+		114	63.2	48.9	0.0088
	10	+		255	63.1	23.1	<0.001
	71	+		233	60.9	37.0	<0.001
	90			333	53.8	-	-
20	74	-		40	27.5	57.3	<0.001

Table 20. Correlation Between L90M, Secondary Mutations, and Saquinavir Susceptibility (fold change threshold > 2.5).

	position	+	or -	n	mt % >2.5	wt % >2.5	p value
25	53	+		29	100.0	77.3	<0.001
	66	+		13	100.0	78.4	0.0459
	84	+		104	98.1	70.7	<0.001
30	54	+		129	96.9	68.1	<0.001
	48	+		22	95.5	78.1	0.0362
	33	+		37	94.6	77.4	0.0076
	73	+		117	89.7	73.6	<0.001
	20	+		115	89.6	73.9	<0.001
35	71	+		233	88.4	58.0	<0.001
	36	+		114	87.7	74.9	0.0038
	10	+		255	86.3	56.4	<0.001
	37	+		104	85.6	76.4	0.0365
	63	+		325	80.3	37.5	0.0112
40	90			333	79.3	-	-
	93	-		187	74.3	85.6	0.0080
	64	-		66	63.6	83.1	<0.001

Table 21. Correlation Between L90M, Secondary Mutations, and Saquinavir Susceptibility (fold change threshold > 10) .

position	+	or -	n	mt % >10	wt %>10	p value
84	+		104	84.6	24.9	<0.001
53	+		29	82.8	39.8	<0.001
48	+		22	81.8	40.8	<0.001
23	+		12	75.0	42.4	0.0260
58	+		30	63.3	41.6	0.0182
20	+		115	61.7	33.9	<0.001
36	+		114	61.4	34.2	<0.001
54	+		129	60.5	32.8	<0.001
35	+		109	53.2	38.8	0.0091
73	+		117	51.3	39.4	0.0240
10	+		255	50.6	20.5	<0.001
71	+		233	49.8	29.0	<0.001
62	+		154	49.4	38.5	0.0306
90			333	43.5		
93	-		187	38.0	50.7	0.0135
77	-		139	35.3	49.5	0.0066
64	-		66	33.3	46.1	0.0409

Table 22. Association Between Saquinavir Susceptibility, L90M, and Number of Resistance Associated Mutations.

Number of secondary mutations	n	% with SQV FC > 2.5	Mean SQV fold change
0	17	23.5	2.4
1	40	25.0	2.4
2	49	69.4	5.4
3	63	85.7	10.0
4	74	97.3	36.6
5	34	100	50.3
6 or more	56	100	94.2

Tables 23-27 show results as indicated using the above procedures as described in Examples 17 and 18.

Table 23. Correlation Between L90M, Secondary Mutations, and Amprenavir Susceptibility (fold change threshold > 2.5).

Amprenavir						
position	+	or -	n	mt % >2.5	wt %>2.5	p value
89	+		11	90.9	59.3	0.0298
53	+		29	89.7	57.6	<0.001
84	+		104	86.5	48.5	<0.001
33	+		37	83.8	57.4	0.0012
92	+		24	83.3	58.6	0.0120
95	+		23	82.6	58.7	0.0174
54	+		129	80.6	47.5	<0.001
58	+		30	76.7	58.7	0.0400
46	+		164	75.0	46.2	<0.001
82	+		135	70.4	53.5	0.0014
36	+		114	70.2	55.3	0.0055
10	+		255	69.4	30.8	<0.001
62	+		154	66.2	55.3	0.0272
90			333	60.4		
74	-		40	45.0	62.5	0.0269
15	-		53	43.4	63.6	0.0050

Table 24. Correlation Between L90M, Secondary Mutations, and Amprenavir Susceptibility (fold change threshold > 10).

Amprenavir						
position	+	or -	n	% >10	wt %>10	p value
47		+	5	80.0	11.9	0.0011
33		+	37	48.6	8.4	<0.001
66		+	13	38.5	11.9	0.0166
32		+	16	37.5	11.7	0.0097
55		+	22	31.8	11.6	0.0140
53		+	29	27.6	11.5	0.0213
54		+	129	24.0	5.9	<0.001
84		+	104	22.1	8.7	0.0010
13		+	77	19.5	10.9	0.0424
46		+	164	17.7	8.3	0.0080
10		+	255	16.1	2.6	<0.001
90			333	12.9		
69	-		37	2.7	14.2	0.0316

Table 25. Correlation Between V82, Secondary Mutations, and Indinavir Susceptibility (fold change threshold > 2.5)

Indinavir						
position	+	or -	n	mt % >2.5	wt %>2.5	p value
84	+		37	100.0	91.0	0.0397
20	+		77	98.7	89.6	0.0064
72	+		56	98.2	90.7	0.0432
54	+		188	97.3	80.5	<0.001
71	+		184	97.3	81.4	<0.001
46	+		157	95.5	87.6	0.0155
93	+		133	95.5	89.1	0.0391
10	+		224	94.6	80.4	0.0034
82			270	92.2		
37	-		108	88.0	95.1	0.0297
64	-		56	85.7	93.9	0.0451
13	-		37	70.3	95.7	<0.001
45	-		12	58.3	93.8	<0.001

Table 26. Correlation Between V82, Secondary Mutations, and Amprenavir Susceptibility (fold change threshold > 2.5)

Amprenavir						
position	+	or -	n	mt % >2.5	wt %>2.5	p value
33	+		24	95.8	56.5	<0.001
23	+		12	91.7	58.5	0.0176
84	+		37	86.5	55.8	<0.001
32	+		24	83.3	57.7	0.0104
53	+		33	81.8	57.0	0.0042
90	+		135	70.4	49.6	<0.001
37	+		108	66.7	55.6	0.0442
71	+		184	66.3	46.5	0.0016
46	+		157	65.6	52.2	0.0184
10	+		224	65.2	34.8	<0.001
54	+		188	63.8	51.2	0.0356
82			270	60.0		
61	-		21	38.1	61.8	0.0297

Table 27. Correlation Between V82, Secondary Mutations, and Amprenavir Susceptibility (fold change threshold > 10).

Amprenavir					
position	+ or -	n	mt % >10	wt % >10	p value
33	+	24	50.0	6.5	<0.001
11	+	8	37.5	9.5	0.0394
84	+	37	35.1	6.4	<0.001
32	+	24	25.0	8.9	0.0258
60	+	30	23.3	8.8	0.0229
53	+	33	21.2	8.9	0.0382
90	+	135	14.8	5.9	0.0133
46	+	157	14.6	4.4	0.0046
71	+	184	13.0	4.7	0.0243
10	+	224	12.5	0.0	0.0039
82		270	10.4		

In Tables 13-27, the first column lists the various codon positions for HIV-1 protease for the secondary mutations and the primary mutation at codon 82 or 90.

The second column represents a positive (+) or negative (-) correlation between the change in resistance from the number of wild-type reference samples to those samples having the secondary mutation.

The fourth column, designates "mt %", as the percentage of samples having the secondary mutation and showing the indicated fold resistance to the specified protease inhibitor, (i.e, > 10 fold or > 2.5 fold).

The fifth column, designates "wt %", as the percentage of wild-type reference samples showing the indicated fold resistance, (i.e, > 10 fold or or 2.5 fold) to the specified protease inhibitor.

The sixth column represents the statistical P value for a correlation.

The following list of mutations represents, by example, secondary mutations from a database for selected patient samples used to establish the above data in Tables 13-27. The mutations listed show the wild type reference amino acid and the possible various mutations for the substituted amino acid at the designated codon position for HIV-1 protease.

5
10 L10F/I/R/V, I13V, K20I/M/R/T/V
L23I, V32I, L33F/I/V
E35/D/N/G, M36I/L/T/V, N37C/D/E/G/H/S/T
P39A/Q/S/T, R41K/W/S, K43R/T
K45R, M46I/L/V, G48M/S/V
15 S53L/Y, I54A/L/M/S/T/V, K55N/R
Q58E, D60E, I62/V/M,
L63A/C/D/S/H/I/N/P/Q/R/S/T/V/Y
I64L/M/V, I66F/L/T/V, A71I/L/T/V
I72A/E/K/L/M/R/T/V, G73A/C/S/T, T74A/K/P/S
20 V77I/T, V82A/F/S/T, I84A/M/V, I85V
L90M, I93L/M, C95F

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